

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 18, 2004, 16:01:00 ; Search time 54 Seconds

(without alignments)  
1752.841 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772  
Sequence: 1 MAGSPCTCLTLYLMQJTG.....PHSLTMPDPRFLFAYENV 335Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

## Database :

A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1772	100.0	335	3	AAV66701
2	1772	100.0	335	3	AAV70431
3	1772	100.0	335	3	AAV44609
4	1772	100.0	335	4	AAU29119
5	1772	100.0	335	4	AAAB87548
6	1772	100.0	335	4	AAAB47321
7	1772	100.0	335	4	ABAB55224
8	1772	100.0	335	5	ABAG58873
9	1772	100.0	335	6	ABUS8495
10	1772	100.0	335	6	ABU88043
11	1772	100.0	335	6	ABU84358
12	1772	100.0	335	6	ABR66232
13	1772	100.0	335	6	ABR65622
14	1772	100.0	335	6	ABU99562
15	1772	100.0	335	6	ABU58039
16	1772	100.0	335	6	ABU59117
17	1772	100.0	335	6	ABU82629
18	1772	100.0	335	6	ABU82801
19	1772	100.0	335	6	ABU89922
20	1772	100.0	335	6	ABR68171
21	1772	100.0	335	6	ABU60548
22	1772	100.0	335	6	ABU96224
23	1772	100.0	335	6	ABU92655
24	1772	100.0	335	6	ABO08732
25	1772	100.0	335	6	ABO02784

26	1772	100.0	335	6	ABR74938	Abx74938 Human sec
27	1772	100.0	335	6	ABR94700	Abx94700 Human sec
28	1772	100.0	335	6	ABU13930	Abu13930 Human PRO
29	1772	100.0	335	6	ABU85673	Abu85673 Human PRO
30	1772	100.0	335	6	ABU98833	Abu98833 Novel hum
31	1772	100.0	335	6	ABU98048	Abu98048 Novel hum
32	1772	100.0	335	6	ABU91754	Abu91754 Novel hum
33	1772	100.0	335	6	ABU89447	Abu89447 Human PRO
34	1772	100.0	335	6	ABU86288	Abu86288 Human sec
35	1772	100.0	335	6	ABU7501	Abu7501 Human sec
36	1772	100.0	335	6	ABU80529	Abu80529 Human PRO
37	1772	100.0	335	6	ABU72515	Abu72515 Novel hum
38	1772	100.0	335	6	ABU90898	Abu90898 Novel hum
39	1772	100.0	335	6	ABO33957	ABO33957 Human sec
40	1772	100.0	335	6	ABR99447	Abx99447 Human sec
41	1772	100.0	335	6	ABR98837	Abx98837 Human sec
42	1772	100.0	335	6	ABO16360	ABO16360 Human sec
43	1772	100.0	335	6	ABR92260	Abx92260 Human sec
44	1772	100.0	335	6	ABO18901	ABO18901 Human sec
45	1772	100.0	335	6	ABR78332	Abx78332 Human sec
46	1772	100.0	335	6	ABU71974	Abu71974 Novel hum
47	1772	100.0	335	6	ABU85058	Abu85058 Novel hum
48	1772	100.0	335	6	ABO00197	ABO00197 Novel hum
49	1772	100.0	335	6	ABO11529	ABO11529 Human sec
50	1772	100.0	335	6	ABO02174	ABO02174 Human sec
51	1772	100.0	335	6	ABU88748	Abu88748 Novel hum
52	1772	100.0	335	6	ABU83443	Abu83443 Human sec
53	1772	100.0	335	6	ABO06244	ABO06244 Novel hum
54	1772	100.0	335	6	ABR95280	Abx95280 Human sec
55	1772	100.0	335	6	ABO09342	ABO09342 Human sec
56	1772	100.0	335	6	ABO19206	ABO19206 Novel hum
57	1772	100.0	335	6	ABO11224	ABO11224 Human sec
58	1772	100.0	335	6	ABR66842	Abx66842 Human sec
59	1772	100.0	335	6	ABO16055	ABO16055 Human sec
60	1772	100.0	335	6	ABO13761	ABO13761 Human sec
61	1772	100.0	335	6	ABU71528	Abu71528 Human sec
62	1772	100.0	335	6	ABU65664	Abu65664 Human sec
63	1772	100.0	335	6	ABO07512	ABO07512 Human PRO
64	1772	100.0	335	6	ABO03699	ABO03699 Human sec
65	1772	100.0	335	6	ABR67147	Abx67147 Human sec
66	1772	100.0	335	6	ABO15750	ABO15750 Human sec
67	1772	100.0	335	6	ABU56031	Abu56031 Human sec
68	1772	100.0	335	6	ABU72309	Abu72309 Human PRO
69	1772	100.0	335	6	ABU65359	Abu65359 Human PRO
70	1772	100.0	335	6	ABU95304	Abu95304 Novel hum
71	1772	100.0	335	6	ABU71207	Abu71207 Human PRO
72	1772	100.0	335	6	ABO07817	ABO07817 Human PRO
73	1772	100.0	335	6	ABR70058	Abx70058 Human sec
74	1772	100.0	335	6	ABR69391	Abx69391 Human sec
75	1772	100.0	335	6	ABO01532	ABO01532 Human PRO
76	1772	100.0	335	6	ABU81334	Abu81334 Human PRO
77	1772	100.0	335	6	ABR60131	Abx60131 Human sec
78	1772	100.0	335	6	ABU90982	Abu90982 Human PRO
79	1772	100.0	335	6	ABR67866	Abx67866 Human sec
80	1772	100.0	335	6	ABR65254	Abx65254 Human sec
81	1772	100.0	335	6	ABR68476	Abx68476 Human sec
82	1772	100.0	335	6	ABR71888	Abx71888 Human sec
83	1772	100.0	335	6	ABU59264	Abu59264 Human sec
84	1772	100.0	335	6	ABU85368	Abu85368 Human PRO
85	1772	100.0	335	6	ABU90958	Abu90958 Human sec
86	1772	100.0	335	6	ABU83138	Abu83138 Human sec
87	1772	100.0	335	6	ABU94994	Abu94994 Novel hum
88	1772	100.0	335	6	ABU90542	Abu90542 Novel hum
89	1772	100.0	335	6	ABU84053	Abu84053 Human sec
90	1772	100.0	335	6	ABU93704	Abu93704 Novel hum
91	1772	100.0	335	6	ABO25961	ABO25961 Human PRO
92	1772	100.0	335	6	ABR64949	Abx64949 Human sec
93	1772	100.0	335	6	ABO27303	ABO27303 Human sec
94	1772	100.0	335	6	ABR68781	Abx68781 Human sec
95	1772	100.0	335	6	ABO06597	ABO06597 Human sec
96	1772	100.0	335	6	ABR99142	Abx99142 Human sec
97	1772	100.0	335	6	ABU57026	Abu57026 Human PRO
98	1772	100.0	335	6	ABU85978	Abu85978 Novel hum

99	1772	100.0	335	6	ABU82265	ABu82265	Novel	hum	172	1772	100.0	335	6	ABO44026	ABo44026	Human	PRO
100	1772	100.0	335	6	ABU87276	ABu87276	Human	PRO	173	1772	100.0	335	6	ADA79944	AdA79944	Human	sec
101	1772	100.0	335	6	ABU83748	ABu83748	Human	sec	174	1772	100.0	335	6	ABM24821	ABm24821	Human	sec
102	1772	100.0	335	6	ABO08122	ABo08122	Human	PRO	175	1772	100.0	335	6	ABO03089	ABo03089	Human	sec
103	1772	100.0	335	6	ABU92812	ABu92812	Human	sec	176	1772	100.0	335	6	ABM19345	ABm19345	Human	sec
104	1772	100.0	335	6	ABU81833	ABu81833	Novel	hum	177	1772	100.0	335	6	ABM17259	ABm17259	Human	sec
105	1772	100.0	335	6	ABU65997	ABu65997	Novel	hum	178	1772	100.0	335	6	ABR95005	ABr95005	Human	sec
106	1772	100.0	335	6	ABU81168	ABu81168	Human	sec	179	1772	100.0	335	6	ABR95310	ABr95310	Human	sec
107	1772	100.0	335	6	ABR59836	ABr59836	Human	sec	180	1772	100.0	335	6	ADB11703	ADb11703	Human	sec
108	1772	100.0	335	6	ABU94014	ABu94014	Novel	hum	181	1772	100.0	335	6	ABO21548	ABo21548	Human	PRO
109	1772	100.0	335	6	ABU99867	ABu99867	Novel	hum	182	1772	100.0	335	6	ABR97812	ABr97812	Human	sec
110	1772	100.0	335	6	ABR66537	ABr66537	Human	sec	183	1772	100.0	335	6	ABR87600	ABr87600	Human	sec
111	1772	100.0	335	6	ABR90955	ABr90955	Human	sec	184	1772	100.0	335	6	ABM17641	ABm17641	Human	sec
112	1772	100.0	335	6	ABO53283	ABo53283	Novel	hum	185	1772	100.0	335	6	ABM27871	ABm27871	Human	sec
113	1772	100.0	335	6	ABU58970	ABu58970	Novel	hum	186	1772	100.0	335	6	ABM06152	ABm06152	Human	sec
114	1772	100.0	335	6	ABU94382	ABu94382	Human	PRO	187	1772	100.0	335	6	ABM03658	ABm03658	Human	sec
115	1772	100.0	335	6	ABU79264	ABu79264	Human	PRO	188	1772	100.0	335	6	ABM35109	ABm35109	Human	sec
116	1772	100.0	335	6	ABU86593	ABu86593	Human	sec	189	1772	100.0	335	6	ABM26346	ABm26346	Human	sec
117	1772	100.0	335	6	ABU86898	ABu86898	Novel	hum	190	1772	100.0	335	6	ABO48128	ABo48128	Human	sec
118	1772	100.0	335	6	ABU94687	ABu94687	Human	PRO	191	1772	100.0	335	6	ABR92870	ABr92870	Human	sec
119	1772	100.0	335	6	ABO04614	ABo04614	Human	PRO	192	1772	100.0	335	6	ABO24631	ABo24631	Human	sec
120	1772	100.0	335	6	ABR70363	ABr70363	Human	sec	193	1772	100.0	335	6	ADA37764	AdA37764	Human	sec
121	1772	100.0	335	6	ABU92348	ABu92348	Novel	hum	194	1772	100.0	335	6	ABM11642	ABm11642	Human	sec
122	1772	100.0	335	6	ABU98328	ABu98328	Human	PRO	195	1772	100.0	335	6	ABM02743	ABm02743	Human	sec
123	1772	100.0	335	6	ABR65927	ABr65927	Human	sec	196	1772	100.0	335	6	ABM16039	ABm16039	Human	sec
124	1772	100.0	335	6	ABR64644	ABr64644	Human	sec	197	1772	100.0	335	6	ABO27600	ABo27600	Human	sec
125	1772	100.0	335	6	ABU59413	ABu59413	Novel	hum	198	1772	100.0	335	6	ABM29091	ABm29091	Human	sec
126	1772	100.0	335	6	ABU79569	ABu79569	Human	PRO	199	1772	100.0	335	6	ABM07067	ABm07067	Human	sec
127	1772	100.0	335	6	ABU92960	ABu92960	Human	sec	200	1772	100.0	335	6	ABM21161	ABm21161	Human	sec
128	1772	100.0	335	6	ABU95919	ABu95919	Human	sec	201	1772	100.0	335	6	ABM09507	ABm09507	Human	sec
129	1772	100.0	335	6	ABU91139	ABu91139	Novel	hum	202	1772	100.0	335	6	ABO41377	ABo41377	Human	sec
130	1772	100.0	335	6	ABU90232	ABu90232	Novel	hum	203	1772	100.0	335	6	ABO36192	ABo36192	Human	PRO
131	1772	100.0	335	6	ABO09647	ABo09647	Human	sec	204	1772	100.0	335	6	ABO43721	ABo43721	Human	PRO
132	1772	100.0	335	6	ABR58417	ABr58417	Human	NOV	205	1772	100.0	335	6	ABM76421	ABm76421	Human	sec
133	1772	100.0	335	6	ABO10919	ABo10919	Human	sec	206	1772	100.0	335	6	ABM76117	ABm76117	Human	sec
134	1772	100.0	335	6	ABR70973	ABr70973	Human	sec	207	1772	100.0	335	6	ABM25736	ABm25736	Human	sec
135	1772	100.0	335	6	ABU98285	ABu98285	Novel	hum	208	1772	100.0	335	6	ABM26041	ABm26041	Human	sec
136	1772	100.0	335	6	ABU87581	ABu87581	Human	PRO	209	1772	100.0	335	6	ADA21450	AdA21450	Human	sec
137	1772	100.0	335	6	ABU91449	ABu91449	Human	PRO	210	1772	100.0	335	6	ABO03394	ABo03394	Human	sec
138	1772	100.0	335	6	ABU89290	ABu89290	Novel	hum	211	1772	100.0	335	6	ABO02479	ABo02479	Human	sec
139	1772	100.0	335	6	ABU84663	ABu84663	Human	sec	212	1772	100.0	335	6	ABO44261	ABo44261	Human	sec
140	1772	100.0	335	6	ABR69753	ABr69753	Human	sec	213	1772	100.0	335	6	ABR90650	ABr90650	Human	sec
141	1772	100.0	335	6	ABU80130	ABu80130	Human	PRO	214	1772	100.0	335	6	ABR73718	ABr73718	Human	sec
142	1772	100.0	335	6	ABU82497	ABu82497	Novel	hum	215	1772	100.0	335	6	ABO16970	ABo16970	Human	sec
143	1772	100.0	335	6	ABU92179	ABu92179	Novel	hum	216	1772	100.0	335	6	ABR94395	ABr94395	Human	sec
144	1772	100.0	335	6	ABU93399	ABu93399	Human	PRO	217	1772	100.0	335	6	ABR75902	ABr75902	Human	sec
145	1772	100.0	335	6	ABO09952	ABo09952	Human	sec	218	1772	100.0	335	6	ABR71278	ABr71278	Human	sec
146	1772	100.0	335	6	ABO09037	ABo09037	Human	sec	219	1772	100.0	335	6	ABR93175	ABr93175	Human	sec
147	1772	100.0	335	6	ABU96461	ABu96461	Human	PRO	220	1772	100.0	335	6	ABR93480	ABr93480	Human	sec
148	1772	100.0	335	6	ABU10885	ABu10885	Human	PRO	221	1772	100.0	335	6	ADA10237	AdA10237	Human	sec
149	1772	100.0	335	6	ABU10605	ABu10605	Human	sec	222	1772	100.0	335	6	ABR87905	ABr87905	Human	sec
150	1772	100.0	335	6	ABU81637	ABu81637	Novel	hum	223	1772	100.0	335	6	ABO27905	ABo27905	Human	sec
151	1772	100.0	335	6	ABU72131	ABu72131	Human	PRO	224	1772	100.0	335	6	ABO30040	ABo30040	Human	sec
152	1772	100.0	335	6	ABU95614	ABu95614	Human	PRO	225	1772	100.0	335	6	ABO33249	ABo33249	Human	PRO
153	1772	100.0	335	6	ABU96823	ABu96823	Novel	hum	226	1772	100.0	335	6	ABM04937	ABm04937	Human	sec
154	1772	100.0	335	6	ABR70668	ABr70668	Human	sec	227	1772	100.0	335	6	ABM08897	ABm08897	Human	sec
155	1772	100.0	335	6	ABO05019	ABo05019	Novel	hum	228	1772	100.0	335	6	ABO36497	ABo36497	Human	sec
156	1772	100.0	335	6	ABO08427	ABo08427	Human	sec	229	1772	100.0	335	6	ABO35582	ABo35582	Human	PRO
157	1772	100.0	335	6	ABU88576	ABu88576	Human	sec	230	1772	100.0	335	6	ABO39547	ABo39547	Human	sec
158	1772	100.0	335	6	ABO34090	ABo34090	Human	PRO	231	1772	100.0	335	6	ABM10422	ABm10422	Human	sec
159	1772	100.0	335	6	ABO05634	ABo05634	Human	sec	232	1772	100.0	335	6	ABM11947	ABm11947	Human	sec
160	1772	100.0	335	6	ABR74023	ABr74023	Human	sec	233	1772	100.0	335	6	ABO52093	ABo52093	Human	PRO
161	1772	100.0	335	6	ABR95615	ABr95615	Human	sec	234	1772	100.0	335	6	ABO52398	ABo52398	Human	PRO
162	1772	100.0	335	6	ABR80912	ABr80912	Human	sec	235	1772	100.0	335	6	ADA19908	AdA19908	Novel	hum
163	1772	100.0	335	6	ABR81217	ABr81217	Human	sec	236	1772	100.0	335	6	ABO23716	ABo23716	Human	sec
164	1772	100.0	335	6	ABM00913	ABm00913	Human	sec	237	1772	100.0	335	6	ABD11791	ABd11791	Human	sec
165	1772	100.0	335	6	ABR88515	ABr88515	Human	sec	238	1772	100.0	335	6	ADA17781	AdA17781	Human	PRO
166	1772	100.0	335	6	ABM77336	ABm77336	Human	sec	239	1772	100.0	335	6	ABR97202	ABr97202	Human	sec
167	1772	100.0	335	6	ABO28820	ABo28820	Human	sec	240	1772	100.0	335	6	ABR86990	ABr86990	Human	sec
168	1772	100.0	335	6	ABO31565	ABo31565	Human	sec	241	1772	100.0	335	6	ABM11032	ABm11032	Human	sec
169	1772	100.0	335	6	ABM07982	ABm07982	Human	sec	242	1772	100.0	335	6	ABM28176	ABm28176	Human	sec
170	1772	100.0	335	6	ABO40462	ABo40462	Human	sec	243	1772	100.0	335	6	ABO32175	ABo32175	Human	sec
171	1772	100.0	335	6	ABO35887	ABo35887	Human	PRO	244	1772	100.0	335	6	ABM15302	ABm15302	Human	sec

245	1772	100.0	335	6	ABM06457	Abm06457	Human	sec	318	1772	100.0	335	6	ABO28515	AbO28515	Human	sec
246	1772	100.0	335	6	ABM04258	Abm04258	Human	sec	319	1772	100.0	335	6	ABO30345	AbO30345	Human	sec
247	1772	100.0	335	6	ABM22381	Abm22381	Human	sec	320	1772	100.0	335	6	ABM07372	AbM07372	Human	sec
248	1772	100.0	335	6	ABM07677	Abm07677	Human	sec	321	1772	100.0	335	6	ABM03963	Abm03963	Human	sec
249	1772	100.0	335	6	ABO40767	AbO40767	Human	sec	322	1772	100.0	335	6	ABO37107	AbO37107	Human	sec
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251	1772	100.0	335	6	ABM31777	Abm31777	Human	sec	324	1772	100.0	335	6	ABO35277	AbO35277	Human	sec
252	1772	100.0	335	6	ABO52703	AbO52703	Human	PRO	325	1772	100.0	335	6	ABM25126	AbM25126	Human	sec
253	1772	100.0	335	6	ABO50263	AbO50263	Human	sec	326	1772	100.0	335	6	ABO47518	AbO47518	Human	sec
254	1772	100.0	335	6	ABU99257	AbU99257	Human	sec	327	1772	100.0	335	6	ABO47823	AbO47823	Human	sec
255	1772	100.0	335	6	ABU04309	AbU04309	Human	sec	328	1772	100.0	335	6	ABO48433	AbO48433	Human	sec
256	1772	100.0	335	6	ABO05939	AbO05939	Human	sec	329	1772	100.0	335	6	ABO51483	AbO51483	Human	PRO
257	1772	100.0	335	6	ABM18479	Abm18479	Human	sec	330	1772	100.0	335	6	ABO51788	AbO51788	Human	PRO
258	1772	100.0	335	6	ADA27889	AdA27889	Human	sec	331	1772	100.0	335	6	ABO50568	AbO50568	Human	sec
259	1772	100.0	335	6	ABR87507	AbR87507	Human	sec	332	1772	100.0	335	6	ABR79692	AbR79692	Human	sec
260	1772	100.0	335	6	ABR80607	AbR80607	Human	sec	333	1772	100.0	335	6	ABM16954	AbM16954	Human	sec
261	1772	100.0	335	6	ABM01218	Abm01218	Human	sec	334	1772	100.0	335	6	ABO17966	AbO17966	Human	sec
262	1772	100.0	335	6	ABR88820	AbR88820	Human	sec	335	1772	100.0	335	6	ABO20938	AbO20938	Human	sec
263	1772	100.0	335	6	ABM13472	Abm13472	Human	sec	336	1772	100.0	335	6	ABR96897	AbR96897	Human	sec
264	1772	100.0	335	6	ABM20856	Abm20856	Human	sec	337	1772	100.0	335	6	ADA38694	AdA38694	Human	sec
265	1772	100.0	335	6	ABO41987	AbO41987	Human	sec	338	1772	100.0	335	6	ABM12252	AbM12252	Human	sec
266	1772	100.0	335	6	ABO42597	AbO42597	Human	sec	339	1772	100.0	335	6	ABM16344	AbM16344	Human	sec
267	1772	100.0	335	6	ABM10117	Abm10117	Human	sec	340	1772	100.0	335	6	ABM24211	AbM24211	Human	sec
268	1772	100.0	335	6	ABO38632	AbO38632	Human	sec	341	1772	100.0	335	6	ABM14692	AbM14692	Human	sec
269	1772	100.0	335	6	ABM32872	Abm32872	Human	sec	342	1772	100.0	335	6	ABM04573	AbM04573	Human	sec
270	1772	100.0	335	6	ABM22686	Abm22686	Human	sec	343	1772	100.0	335	6	ABM06762	AbM06762	Human	sec
271	1772	100.0	335	6	ABM74897	Abm74897	Human	sec	344	1772	100.0	335	6	ABM09202	AbM09202	Human	sec
272	1772	100.0	335	6	ADA79736	AdA79736	Human	sec	345	1772	100.0	335	6	ABO39242	AbO39242	Human	sec
273	1772	100.0	335	6	ABR96287	AbR96287	Human	sec	346	1772	100.0	335	6	ABM75507	AbM75507	Human	sec
274	1772	100.0	335	6	ABM02438	Abm02438	Human	sec	347	1772	100.0	335	6	ABM25431	AbM25431	Human	sec
275	1772	100.0	335	6	ABR86380	AbR86380	Human	sec	348	1772	100.0	335	6	ABM19941	AbM19941	Human	sec
276	1772	100.0	335	6	ABR86685	AbR86685	Human	sec	349	1772	100.0	335	6	ABO466847	AbO466847	Human	PRO
277	1772	100.0	335	6	ABM16649	Abm16649	Human	sec	350	1772	100.0	335	6	ABO47152	AbO47152	Human	PRO
278	1772	100.0	335	6	ABM29701	Abm29701	Human	sec	351	1772	100.0	335	6	ADA83261	AdA83261	Human	sec
279	1772	100.0	335	6	ABO29125	AbO29125	Human	sec	352	1772	100.0	335	6	ABR71583	AbR71583	Human	sec
280	1772	100.0	335	6	ABM23906	Abm23906	Human	sec	353	1772	100.0	335	6	ABR72193	AbR72193	Human	sec
281	1772	100.0	335	6	ABM23296	Abm23296	Human	sec	354	1772	100.0	335	6	ABR98532	AbR98532	Human	sec
282	1772	100.0	335	6	ABM22076	Abm22076	Human	sec	355	1772	100.0	335	6	ABO06902	AbO06902	Human	sec
283	1772	100.0	335	6	ABO37717	AbO37717	Human	sec	356	1772	100.0	335	6	ABR84855	AbR84855	Human	sec
284	1772	100.0	335	6	ABM28481	Abm28481	Human	sec	357	1772	100.0	335	6	ABR73413	AbR73413	Human	sec
285	1772	100.0	335	6	ABM28786	Abm28786	Human	sec	358	1772	100.0	335	6	ABR76507	AbR76507	Human	sec
286	1772	100.0	335	6	ABM66430	Abm66430	Human	sec	359	1772	100.0	335	6	ABR73108	AbR73108	Human	sec
287	1772	100.0	335	6	ABM75812	Abm75812	Human	sec	360	1772	100.0	335	6	ABM18174	AbM18174	Human	sec
288	1772	100.0	335	6	ABM34092	Abm34092	Human	sec	361	1772	100.0	335	6	ABO20633	AbO20633	Human	sec
289	1772	100.0	335	6	ABM34397	Abm34397	Human	sec	362	1772	100.0	335	6	ABO25376	AbO25376	Human	PRO
290	1772	100.0	335	6	ABO20328	AbO20328	Human	sec	363	1772	100.0	335	6	ABO25681	AbO25681	Human	PRO
291	1772	100.0	335	6	ABO21243	AbO21243	Human	sec	364	1772	100.0	335	6	ABR94090	AbR94090	Human	sec
292	1772	100.0	335	6	ABO22158	AbO22158	Human	sec	365	1772	100.0	335	6	ADA92815	AdA92815	Human	sec
293	1772	100.0	335	6	ADA20080	AdA20080	Novel	hum	366	1772	100.0	335	6	ABR79997	AbR79997	Human	sec
294	1772	100.0	335	6	ABO34189	AbO34189	Human	sec	367	1772	100.0	335	6	ABM11337	AbM11337	Human	sec
295	1772	100.0	335	6	ABR96592	AbR96592	Human	sec	368	1772	100.0	335	6	ABO32994	AbO32994	Human	PRO
296	1772	100.0	335	6	ADA94469	AdA94469	Human	sec	369	1772	100.0	335	6	ABO30650	AbO30650	Human	sec
297	1772	100.0	335	6	ABR85770	AbR85770	Human	sec	370	1772	100.0	335	6	ABO30955	AbO30955	Human	sec
298	1772	100.0	335	6	ABR99752	AbR99752	Human	sec	371	1772	100.0	335	6	ABM27261	AbM27261	Human	sec
299	1772	100.0	335	6	ABM06068	Abm06068	Human	sec	372	1772	100.0	335	6	ABM30006	AbM30006	Human	sec
300	1772	100.0	335	6	ABM00303	Abm00303	Human	sec	373	1772	100.0	335	6	ABM05542	AbM05542	Human	sec
301	1772	100.0	335	6	ABO29735	AbO29735	Human	sec	374	1772	100.0	335	6	ABM15607	AbM15607	Human	sec
302	1772	100.0	335	6	ABM23601	Abm23601	Human	sec	375	1772	100.0	335	6	ABM08592	AbM08592	Human	sec
303	1772	100.0	335	6	ABM29396	Abm29396	Human	sec	376	1772	100.0	335	6	ABO42292	AbO42292	Human	sec
304	1772	100.0	335	6	ABO38327	AbO38327	Human	sec	377	1772	100.0	335	6	ABO38022	AbO38022	Human	sec
305	1772	100.0	335	6	ABO45627	AbO45627	Human	PRO	378	1772	100.0	335	6	ABO45932	AbO45932	Human	PRO
306	1772	100.0	335	6	ABM20551	Abm20551	Human	sec	379	1772	100.0	335	6	ABM66735	AbM66735	Human	sec
307	1772	100.0	335	6	ADA81463	AdA81463	Human	sec	380	1772	100.0	335	6	AD820304	AdB20304	Human	sec
308	1772	100.0	335	6	ABO16665	AbO16665	Human	sec	381	1772	100.0	335	6	ABM19636	Abm19636	Human	sec
309	1772	100.0	335	6	ABO18291	AbO18291	Human	sec	382	1772	100.0	335	6	ABO49348	AbO49348	Human	sec
310	1772	100.0	335	6	ABO22718	AbO22718	Human	PRO	383	1772	100.0	335	6	ABO49653	AbO49653	Human	sec
311	1772	100.0	335	6	ABO23023	AbO23023	Human	PRO	384	1772	100.0	335	6	ADA78556	AdA78556	Human	sec
312	1772	100.0	335	6	ABR92565	AbR92565	Human	sec	385	1772	100.0	335	6	ABR888210	AbR88210	Human	sec
313	1772	100.0	335	6	ABR81522	AbR81522	Human	sec	386	1772	100.0	335	6	ADA00377	AdA00377	Human	sec
314	1772	100.0	335	6	ABR77946	AbR77946	Human	sec	387	1772	100.0	335	6	ABM26956	Abm26956	Human	sec
315	1772	100.0	335	6	ABR89735	AbR89735	Human	sec	388	1772	100.0	335	6	ABM03353	AbM03353	Human	sec
316	1772	100.0	335	6	ABM26651	Abm26651	Human	sec	389	1772	100.0	335	6	ABO39852	AbO39852	Human	sec
317	1772	100.0	335	6	ABM13777	Abm13777	Human	sec	390	1772	100.0	335	7	ABO49958	AbO49958	Human	sec

391	1772	100.0	335	7	ABO50873	AbO50873	Human	sec	464	1772	100.0	335	7	ABM22991	Abm22991	Human	sec
392	1772	100.0	335	7	ABO05329	AbO05329	Human	sec	465	1772	100.0	335	7	ABM30311	Abm30311	Human	sec
393	1772	100.0	335	7	ABR74633	AbR74633	Human	sec	466	1772	100.0	335	7	ABM21771	Abm21771	Human	sec
394	1772	100.0	335	7	ABR77112	AbR77112	Human	sec	467	1772	100.0	335	7	ABM21466	Abm21466	Human	sec
395	1772	100.0	335	7	ABM17869	AbM17869	Human	sec	468	1772	100.0	335	7	ABM14997	Abm14997	Human	sec
396	1772	100.0	335	7	ABR95920	AbR95920	Human	sec	469	1772	100.0	335	7	ABO41072	AbO41072	Human	sec
397	1772	100.0	335	7	ABO21853	AbO21853	Human	sec	470	1772	100.0	335	7	ABO36802	AbO36802	Human	sec
398	1772	100.0	335	7	ABO20023	AbO20023	Human	sec	471	1772	100.0	335	7	ABO37412	AbO37412	Human	sec
399	1772	100.0	335	7	ABO24336	AbO24336	Human	sec	472	1772	100.0	335	7	ABM75202	AbM75202	Human	sec
400	1772	100.0	335	7	ABR86075	AbR86075	Human	sec	473	1772	100.0	335	7	ABM33482	AbM33482	Human	sec
401	1772	100.0	335	7	ABM10727	AbM10727	Human	sec	474	1772	100.0	335	7	ABO46237	AbO46237	Human	sec
402	1772	100.0	335	7	ABM76726	AbM76726	Human	sec	475	1772	100.0	335	7	AD882627	AD882627	Human	sec
403	1772	100.0	335	7	ABR89430	AbR89430	Human	sec	476	1772	100.0	335	7	AD885619	AD885619	Human	sec
404	1772	100.0	335	7	ABM12557	AbM12557	Human	sec	477	1772	100.0	335	7	ADB96261	ADb96261	Human	sec
405	1772	100.0	335	7	ABM05847	AbM05847	Human	sec	478	1772	100.0	335	7	ABM31836	AbM31836	Human	sec
406	1772	100.0	335	7	ABO34972	AbO34972	Human	PRO	479	1772	100.0	335	7	ABM31226	Abm31226	Human	sec
407	1772	100.0	335	7	ABM03048	AbM03048	Human	sec	480	1772	100.0	335	7	AD885935	AD885935	Human	sec
408	1772	100.0	335	7	ABM19026	AbM19026	Human	sec	481	1772	100.0	335	7	ABM32141	Abm32141	Human	sec
409	1772	100.0	335	7	ABM19331	AbM19331	Human	sec	482	1772	100.0	335	7	ABM32446	AbM32446	Human	sec
410	1772	100.0	335	7	ABO46542	AbO46542	Human	PRO	483	1772	100.0	335	7	ADB68298	ADb68298	Human	PRO
411	1772	100.0	335	7	ABO49043	AbO49043	Human	sec	484	1772	100.0	335	7	ADB68105	ADb68105	Human	PRO
412	1772	100.0	335	7	ABR69086	AbR69086	Human	sec	485	1772	100.0	335	7	ABM31531	Abm31531	Human	PRO
413	1772	100.0	335	7	ABR89125	AbR89125	Human	sec	486	1772	100.0	335	7	ABM30921	Abm30921	Human	sec
414	1772	100.0	335	7	ABR72498	AbR72498	Human	sec	487	1772	100.0	335	7	ADB90922	ADb90922	Human	sec
415	1772	100.0	335	7	ABO14338	AbO14338	Human	sec	488	1772	100.0	335	7	ADC57733	ADC57733	Human	PRO
416	1772	100.0	335	7	ABO18596	AbO18596	Human	sec	489	1772	100.0	335	7	ADC55097	ADC55097	Human	PRO
417	1772	100.0	335	7	ABR80302	AbR80302	Human	sec	490	1772	100.0	335	7	ADC11964	ADC11964	Human	sec
418	1772	100.0	335	7	ABM01523	AbM01523	Human	sec	491	1772	100.0	335	7	ADC07002	ADC07002	Human	PRO
419	1772	100.0	335	7	ABM02133	AbM02133	Human	sec	492	1772	100.0	335	7	ADC56386	ADC56386	Human	PRO
420	1772	100.0	335	7	ABR87295	AbR87295	Human	sec	493	1772	100.0	335	7	ADC11781	ADC11781	Mammalian	
421	1772	100.0	335	7	ABM12862	AbM12862	Human	sec	494	1772	100.0	335	7	ADC07441	ADC07441	Human	sec
422	1772	100.0	335	7	ABM30616	AbM30616	Human	sec	495	1772	100.0	335	7	ADC01431	ADC01431	Human	sec
423	1772	100.0	335	7	ABM24516	AbM24516	Human	sec	496	1772	100.0	335	7	ADC14879	ADC14879	Human	sec
424	1772	100.0	335	7	ABO29430	AbO29430	Human	sec	497	1772	100.0	335	7	ADC52374	ADC52374	Human	hum
425	1772	100.0	335	7	ABO31260	AbO31260	Human	sec	498	1772	100.0	335	7	ADC14553	ADC14553	Novel	hum
426	1772	100.0	335	7	ABM14367	AbM14367	Human	sec	499	1772	100.0	335	7	ADD08085	ADD08085	Human	hum
427	1772	100.0	335	7	ABM09812	AbM09812	Human	sec	500	1772	100.0	335	7	ADC81910	ADC81910	Human	PRO
428	1772	100.0	335	7	ABO38937	AbO38937	Human	sec	501	1772	100.0	335	7	ADD07552	ADD07552	Novel	hum
429	1772	100.0	335	7	ABM34702	AbM34702	Human	sec	502	1772	100.0	335	7	ADC82443	ADC82443	Human	PRO
430	1772	100.0	335	7	ABO51178	AbO51178	Human	sec	503	1772	100.0	335	7	ADD05665	ADD05665	Human	sec
431	1772	100.0	335	7	ABO04004	AbO04004	Human	sec	504	1772	100.0	335	7	ADD06623	ADD06623	Human	hum
432	1772	100.0	335	7	ABO10474	AbO10474	Human	PRO	505	1772	100.0	335	7	ADD06872	ADD06872	Novel	hum
433	1772	100.0	335	7	ABO53176	AbO53176	Human	sec	506	1772	100.0	335	7	ADC89503	ADC89503	Human	nat
434	1772	100.0	335	7	ABR77171	AbR77171	Human	sec	507	1772	100.0	335	7	ADC83119	ADC83119	Human	PRO
435	1772	100.0	335	7	ABR78927	AbR78927	Human	sec	508	1772	100.0	335	7	ADD67525	ADD67525	Human	PRO
436	1772	100.0	335	7	ABO24021	AbO24021	Human	sec	509	1772	100.0	335	7	ADD55226	ADD55226	Human	PRO
437	1772	100.0	335	7	ABR93785	AbR93785	Human	sec	510	1772	100.0	335	7	ADD36050	ADD36050	Novel	hum
438	1772	100.0	335	7	ABM01828	AbM01828	Human	sec	511	1772	100.0	335	7	ADD56184	ADD56184	Human	PRO
439	1772	100.0	335	7	ABM78251	AbM78251	Human	sec	512	1772	100.0	335	7	ADD54622	ADD54622	Human	PRO
440	1772	100.0	335	7	ABR90040	AbR90040	Human	sec	513	1772	100.0	335	7	ADBE26776	ADBE26776	Novel	hum
441	1772	100.0	335	7	ADA22376	AdA22376	Human	sec	514	1772	100.0	335	7	ADBE26243	ADBE26243	Novel	hum
442	1772	100.0	335	7	ABM27566	AbM27566	Human	sec	515	1772	100.0	335	8	ADC52184	ADC52184	Novel	hum
443	1772	100.0	335	7	ABM13167	AbM13167	Human	sec	516	1772	100.0	335	8	ADBE74329	ADBE74329	Novel	hum
444	1772	100.0	335	7	ABO31870	AbO31870	Human	sec	517	1772	100.0	335	8	ADBE74941	ADBE74941	Human	sec
445	1772	100.0	335	7	ABM14082	AbM14082	Human	sec	518	1772	100.0	335	8	ADBE74941	ADBE74941	Human	sec
446	1772	100.0	335	7	ABM08287	AbM08287	Human	sec	519	1769	99.8	336	3	AA332373	AA332373	Human	sec
447	1772	100.0	335	7	ABO40157	AbO40157	Human	sec	520	1755.5	99.1	348	6	ABR58418	ABR58418	Human	dis
448	1772	100.0	335	7	ABM74592	AbM74592	Human	sec	521	1653	93.3	312	5	AAV44610	AAV44610	Human	NOV
449	1772	100.0	335	7	ABM33787	AbM33787	Human	sec	522	1392.5	78.6	328	5	ABR97473	ABR97473	Novel	hu
450	1772	100.0	335	7	ABM20246	AbM20246	Human	sec	523	933.5	52.7	684	4	ABG11697	ABG11697	Novel	hum
451	1772	100.0	335	7	ABM02878	AbM02878	Human	sec	524	933.5	52.7	684	4	ABG11697	ABG11697	Novel	hum
452	1772	100.0	335	7	ABO22546	AbO22546	Human	sec	525	612	35.1	124	2	AAV12645	AAV12645	Human	5'
453	1772	100.0	335	7	ABR72803	AbR72803	Human	sec	526	562	32.8	110	2	AAW67811	AAW67811	Human	sec
454	1772	100.0	335	7	ABO15445	AbO15445	Human	sec	527	582	32.8	110	3	AA332405	AA332405	Human	sec
455	1772	100.0	335	7	ABR85160	AbR85160	Human	sec	528	582	32.8	110	6	ADA57321	ADA57321	Human	sec
456	1772	100.0	335	7	ABO15140	AbO15140	Human	sec	529	582	32.8	110	6	ADA56750	ADA56750	Human	sec
457	1772	100.0	335	7	ABO17275	AbO17275	Human	sec	530	582	32.8	110	6	ADA40601	ADA40601	Human	sec
458	1772	100.0	335	7	ABM17564	AbM17564	Human	sec	531	582	32.8	110	6	ADA41198	ADA41198	Human	sec
459	1772	100.0	335	7	ADA06542	AdA06542	Human	sec	532	498	28.1	98	2	AA300391	AA300391	Human	sec
460	1772	100.0	335	7	ADA39235	AdA39235	Human	sec	533	498	28.1	98	2	AAV11662	AAV11662	Human	5'
461	1772	100.0	335	7	ABR85465	AbR85465	Human	sec	534	471	26.6	91	4	AAW21122	AAW21122	Peptide	#
462	1772	100.0	335	7	ABM77031	AbM77031	Human	sec	535	471	26.6	91	4	AB343438	AB343438	Peptide	#
463	1772	100.0	335	7	ABO28210	AbO28210	Human	sec	536	471	26.6	91	4	AAW37326	AAW37326	Peptide	#



537	471	26.6	91	4	ABB26408	Abb26408	Protein #	610	311	17.6	332	8	AD877312	Ad877312	Human sec
538	471	26.6	91	4	AAW7190	Aam7190	Human bon	611	311	17.6	332	8	AD865420	Ad865420	Human PRO
539	471	26.6	91	4	AAW64367	Aam64367	Human bta	612	311	17.6	332	8	AD876029	Ad876029	Human PRO
540	471	26.6	91	4	ABG58815	Abg58815	Human liv	613	311	17.6	332	8	AD837940	Ad837940	Human PRO
541	471	26.6	91	5	ABG46203	Abg46203	Human pep	614	311	17.6	332	8	AD864550	Ad864550	Human PRO
542	445	25.1	90	3	AA832404	Aab32404	Human sec	615	311	17.6	332	8	AD838885	Ad838885	Human PRO
543	362.5	20.5	328	5	AA847878	Aab47878	SCZ/CD84	616	311	17.6	332	8	AD851959	Ad851959	Human sec
544	362.5	20.5	328	5	AA826238	Aae26238	Human CD8	617	311	17.6	332	8	ADD90990	Ad890990	Human sec
545	362.5	20.5	329	2	AAW74891	Aaw74891	Human CD8	618	311	17.6	332	8	AD838769	Ad838769	Human PRO
546	362.5	20.5	329	5	ABG95343	Abg95343	Human sec	619	311	17.6	332	8	AD837469	Ad837469	Human sec
547	362.5	20.5	329	6	ABO34537	AbO34537	Region of	620	311	17.6	332	8	AD806286	Ad806286	Human PRO
548	343	19.4	629	5	AAU74424	Aau74424	Mouse pro	621	311	17.6	332	8	ADD90145	Ad890145	Human sec
549	333.5	18.8	289	5	AA826250	Aae26250	Human CD2	622	311	17.6	332	8	AD838653	Ad838653	Human PRO
550	330.5	18.7	289	4	AA812078	Aae12078	Dendritic	623	311	17.6	332	8	AD839584	Ad839584	Human PRO
551	330.5	18.7	289	5	AA826243	Aae26243	Human CD2	624	311	17.6	332	8	AD889189	Ad889189	Human PRO
552	330.5	18.7	289	5	AA826253	Aae26253	Human CD2	625	311	17.6	332	8	AD888956	Ad888956	Human PRO
553	330.5	18.7	289	5	ABP65110	Abp65110	Hypoxia-1	626	311	17.6	332	8	AD819850	Ad819850	Human PRO
554	327.5	18.5	289	5	AA826251	Aae26251	Human CD2	627	311	17.6	332	8	AD877428	Ad877428	Human sec
555	327.5	18.5	289	5	AA826252	Aae26252	Human CD2	628	311	17.6	332	8	AD865304	Ad865304	Human PRO
556	327.5	18.5	270	5	AA826244	Aae26244	Human CD2	629	311	17.6	332	8	AD839352	Ad839352	Human PRO
557	319.5	18.0	331	5	AA826239	Aae26239	Human CD2	630	311	17.6	332	8	AD838537	Ad838537	Human sec
558	315.5	17.8	309	5	AA826222	Aae26222	Human CD2	631	301.5	17.0	236	5	AA826249	Ad826249	Human CD2
559	315.5	17.8	331	5	AB890183	Abb90183	Human pol	632	298	16.8	217	5	AA826246	Ad826246	Human CD2
560	315.5	17.8	331	5	AA826230	Aae26230	Human CD2	633	294.5	16.6	551	5	ABG96270	Ad896270	Human imm
561	315.5	17.8	331	6	ABR39107	Abc39107	Human NTR	634	251	14.2	220	5	AAU09867	Ad89867	Human pol
562	315.5	17.8	331	6	ABU03145	Abu03145	Human imm	635	247	13.9	310	5	AB853269	Abb53269	Human pol
563	315.5	17.8	331	7	ADCS2556	Adcs2556	human den	636	245	13.8	195	5	AA826231	Ad826231	Human CD2
564	315.5	17.8	346	5	AAU09868	Aau09868	Novel hum	637	245	13.8	203	5	AA826232	Ad826232	Human CD2
565	314.5	17.7	331	5	AA826241	Aae26241	Human CD2	638	236.5	13.3	229	5	AB853268	Abb53268	Human pol
566	314.5	17.7	331	5	AA826240	Aae26240	Human CD2	639	225.5	12.7	351	4	AA847322	Abb47322	APEX-2
567	312.5	17.6	610	5	AAU74425	Aau74425	Human pro	640	219	12.4	168	5	AB889245	Abb89245	Human pol
568	311.5	17.6	331	4	AA826242	Aae26242	Human CD2	641	206	11.6	220	6	ABU03171	Abu03171	Human imm
569	311	17.6	332	4	AA826243	Aae26243	Human CD2	642	200.5	11.3	159	5	AA826225	Ad826225	Human CD2
570	311	17.6	332	5	ABG96267	Abg96267	Human imm	643	199.5	11.3	241	5	ABG96266	Ad896266	Human imm
571	311	17.6	332	5	ABG34067	Abg34067	Human pro	644	186	10.5	323	2	AA897632	Ad897632	Human SLA
572	311	17.6	332	6	ABU03170	Abu03170	Human imm	645	182.5	10.3	335	2	AA897628	Ad897628	Human SLA
573	311	17.6	332	6	ADA37159	Ada37159	Human PRO	646	182.5	10.3	335	4	AA871853	Ad871853	Human SLA
574	311	17.6	332	6	ADA01344	Ada01344	Human PRO	647	182.5	10.3	335	5	AAU11927	Ad811927	Human pro
575	311	17.6	332	6	ADA43773	Ada43773	Human sec	648	182.5	10.3	335	5	AB890776	Abb90776	Human Tum
576	311	17.6	332	6	ADA43541	Ada43541	Human sec	649	182.5	10.3	335	6	AB854483	Abb54483	Human not
577	311	17.6	332	6	ADA01216	Ada01216	Human PRO	650	181.5	10.2	334	5	AA877978	Ad877978	Human b1g
578	311	17.6	332	7	ADA01100	Ada01100	Human sec	651	180	10.2	307	2	AA897631	Ad897631	Human SLA
579	311	17.6	332	7	ADA43657	Ada43657	Human sec	652	179	10.1	278	6	AA892181	Ad892181	Human TRA
580	311	17.6	332	7	ADA06919	Ada06919	Human PRO	653	179	10.1	278	6	ABG74266	Abg74266	Human tra
581	311	17.6	332	7	ADA08407	Ada08407	Novel hum	654	179	10.1	278	7	ABW01426	Abw01426	Human TRA
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584	311	17.6	332	7	AD866138	Adb66138	Human sec	657	170	9.6	365	4	AAV43138	Adv43138	Human NAI
585	311	17.6	332	7	AD899816	Adb99816	Human PRO	658	170	9.6	365	4	AAW23942	Adw23942	Human EST
586	311	17.6	332	7	AD899471	Adb99471	Novel hum	659	170	9.6	365	5	AAU11929	Adu11929	Human pro
587	311	17.6	332	7	AD866022	Adb66022	Human sec	660	170	9.6	391	5	ABP41447	Abp41447	Human ova
588	311	17.6	332	7	AD866022	Adb66022	Human sec	661	164.5	9.3	305	2	AA897630	Ad897630	Human SLA
589	311	17.6	332	7	AD866022	Adb66022	Human tra	662	164.5	9.3	305	6	AB890777	Abb90777	Human Tum
590	311	17.6	332	7	AD866022	Adb66022	Human PRO	663	164.5	9.3	305	6	AB890777	Abb90777	Human not
591	311	17.6	332	7	AD866022	Adb66022	Human PRO	664	158.5	8.9	329	2	AA897633	Ad897633	Human pol
592	311	17.6	332	7	AD866022	Adb66022	Human PRO	665	158.5	8.9	329	2	AA897633	Ad897633	Human SLA
593	311	17.6	332	7	AD866022	Adb66022	Human PRO	666	152	8.6	298	2	AAU11928	Adu11928	Mouse pro
594	311	17.6	332	7	AD866022	Adb66022	Human sec	667	152	8.6	298	2	AA897629	Ad897629	Human SLA
595	311	17.6	332	7	AD866022	Adb66022	Human PRO	668	152	8.6	298	6	AB890778	Abb90778	Human Tum
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597	311	17.6	332	7	AD866022	Adb66022	Human PRO	670	150.5	8.5	285	4	AA897629	Ad897629	Human D-S
598	311	17.6	332	7	AD866022	Adb66022	Human sec	671	150.5	8.5	285	4	AA897629	Ad897629	Human pol
599	311	17.6	332	7	AD866022	Adb66022	Human sec	672	150.5	8.5	285	4	AA897629	Ad897629	Human D-S
600	311	17.6	332	7	AD866022	Adb66022	Human sec	673	150.5	8.5	285	4	AA897629	Ad897629	Human D-S
601	311	17.6	332	7	AD866022	Adb66022	Human sec	674	150.5	8.5	285	4	AA897629	Ad897629	Human D-S
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603	311	17.6	332	7	AD866022	Adb66022	Human sec	676	150.5	8.5	285	4	AA897629	Ad897629	Human D-S
604	311	17.6	332	7	AD866022	Adb66022	Human sec	677	146.5	8.3	211	7	ABW01429	Abw01429	Human tra
605	311	17.6	332	7	AD866022	Adb66022	Human PRO	678	146	8.2	312	3	AA897629	Ad897629	Human tra
606	311	17.6	332	7	AD866022	Adb66022	Human PRO	679	146	8.2	312	6	ABG74265	Abg74265	Human tra
607	311	17.6	332	7	AD866022	Adb66022	Human PRO	680	146	8.2	312	6	ABG74265	Abg74265	Human tra
608	311	17.6	332	7	AD866022	Adb66022	Human PRO	681	146	8.2	318	4	AAW24013	Adw24013	Human EST
609	311	17.6	332	7	AD866022	Adb66022	Human PRO	682	146	8.2	320	3	AA897629	Ad897629	Human par

663 146 8.2 320 6 ABG74267 Human tta  
664 146 8.2 320 7 ABW01436 Human TAN  
665 144.5 8.2 285 3 AAY92183 Aay92183 Full-length  
666 144.5 8.2 285 6 ABG74268  
667 144.5 8.2 285 7 ABW01442  
668 141 8.0 149 7 ADW07622 Human TAN  
669 140.5 7.9 142 6 ADA57556 Human sec  
690 140.5 7.9 142 6 ADA41448 Human sec  
691 140.5 7.9 142 7 ADC74567 Human sec  
692 140.5 7.9 142 7 ADD38086 Human sec  
693 140.5 7.9 143 2 AAY02652 Human sec  
694 140.5 7.9 143 7 ADW07371 Human sec  
695 140.5 7.9 290 7 ABW01419 Human TAN  
696 140.5 7.9 298 7 ABW01438 Human TAN  
697 139 7.8 28 2 AAW67932 Fragment  
698 139 7.8 263 7 ABW01444 Human TAN  
699 138 7.8 70 5 AAE26255 Human CD2  
700 136.5 7.7 351 3 AAY83135 Human CD2

## ALIGNMENTS

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RESULT 1
AAY66701
ID AAY66701 standard; protein; 335 AA.
XX
AC AAY66701;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1138.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN WO963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1999; 98US-0087607P.
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PR 03-JUN-1999; 98US-0087827P.
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 PR 12-JAN-1999: 99US-0115565P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WJ, Yuan J;  
 XX  
 DR MPI: 2000-072863/06.  
 DR N-PSDB; AA265040.  
 XX  
 PT Membrane-bound proteins and related nucleotide sequences.  
 XX  
 PS Clain 12; Fig 171; 822pp; English.  
 XX  
 CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
 CC also be useful for the preparation of PRO polypeptides, especially by  
 CC recombinant techniques  
 CC  
 XX  
 SQ Sequence 335 AA;

Query Match 100.0%; Score 1772; DB 3; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 6, 9e-163;  
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MAGSPCTLTLYILYLMOLGSAAGPYKELVGSYGAVTPPLSKKQVDSIVTFTPTPL 60  
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DB 61 VTIQPEGGTTITVQNRRERVDPPDGYSLSKLSKLKKNNSGIYVVGIVSSSLQGPSTQEX 120  
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 DB 121 VLAHYEHLSPKPYTMGLQSNKNGTCYTNLTCCMEHGESEVITYTWKLAGAANESHNGSL 180  
 QY 181 PISMRGSDMTFICARNPVSRNFSPIARLCEGADDPSSVLLCLLVPPLLSL 240  
 DB 181 PISMRGSDMTFICARNPVSRNFSPIARLCEGADDPSSVLLCLLVPPLLSL 240  
 QY 241 FVLGLFLMFLAKREOREYIEKKRVDICRETPNICPHSGENTERYDTPHTNRITLKEDA 300  
 DB 241 FVLGLFLMFLAKREOREYIEKKRVDICRETPNICPHSGENTERYDTPHTNRITLKEDA 300  
 QY 301 NTVYSTVEIIPKQENPHSLITMPDTPRLFAVENVI 335  
 DB 301 NTVYSTVEIIPKQENPHSLITMPDTPRLFAVENVI 335

## RESULT 2

AA70431 standard; protein; 335 AA.

AA70431;

21-JUN-2000 (first entry)

Human cell surface immunomodulator-1 (CSIMM-1).

KW Cell surface immunomodulator-1; CSIMM-1; cell proliferation; CD84;  
 KW differentiation; signal transduction; drug screening; prevention;  
 KW treatment; cancer; leukaemia; melanoma; immune disorder; AIDS;  
 KW rheumatoid arthritis; asthma; atherosclerosis; diabetes mellitus;  
 KW emphysema; irritable bowel syndrome; multiple sclerosis; diagnosis;  
 KW osteoporosis; psoriasis; microbial infections; cytostatic; antiarthritic;  
 KW antiasthmatic; immunosuppressive; antiarteriosclerotic; anti-HIV;  
 KW antidiabetic; antiinflammatory; neuroprotective; osteopathic;  
 KW antiproliferative; antimicrobial; human.

OS Homo sapiens.

Key Location/Qualifiers

FT 1..22 /label= Signal\_peptide

FT 23..335 /label= Mature\_CSIMM-1

FT 34..107 /note= "Homologous to immunoglobulin domain"

FT 89 /note= "Potential Protein kinase C phosphorylation site"

FT 98 /note= "Potential N-glycosylation site"

FT 103 /note= "Potential tyrosine kinase phosphorylation site"

FT 139 /note= "Potential Casein kinase II phosphorylation site"

FT 142 /note= "Potential Protein kinase C phosphorylation site"

FT 148 /note= "Potential N-glycosylation site"

FT 163 /note= "Potential N-glycosylation site"

FT 172 /note= "Potential Protein kinase C phosphorylation site"

FT 176 /note= "Potential N-glycosylation site"

FT 183 /note= "Potential N-glycosylation site"

FT 204 /note= "Potential Protein kinase C phosphorylation site"

FT /note= "Potential N-glycosylation site"

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PD				
PD	02-MAR-2000.			
XX				
PF	24-AUG-1999;	99WO-US019386.		
XX				
PR	25-AUG-1998;	98US-00155261.		
XX				
PA	(INCY-) INCYTE PHARM INC.			
PI				
XX	Lal P, Corley NC, Gorgone GA, Guejler KU, Patterson C, Baughn MR,			
DR	WPI; 2000-246561/21.			
DR	N-PSDB; AAZ51572.			
XX				
PT	New human cell surface immunomodulatory polypeptides and polynucleotides			
PT	useful for diagnosis, prevention and treatment of cancer and immune			
PT	disorders.			
XX				
PS	Claim 1; Page 61-62; 70pp; English.			
XX				
CC	The present sequence is the human cell surface immunomodulator-1 (CSIM-			
CC	1), which is a regulator of cell proliferation, differentiation, cell-			
CC	cell communication and signal transduction. It is encoded by cDNA			
CC	identified in Inocyte clone 14448, derived from human promonocyte cell			
CC	line (THP-1) cDNA library (THP1P801). It shows homology to cell surface			
CC	antigen, CD84. CSIM can be used for drug screening, prevention and			
CC	treatment of cancers such as leukemia and melanoma, immune disorders			
CC	such as AIDS, rheumatoid arthritis, asthma, atherosclerosis, diabetes			
CC	mellitus, emphysema, irritable bowel syndrome, multiple sclerosis,			
CC	osteoporosis, psoriasis and microbial infections. CSIM polynucleotide			
CC	may be used for diagnosis of CSIM-associated diseases and as source of			
CC	probes useful in mapping naturally occurring genomic sequences			
XX				
XX	Sequence 335 AA;			

[illegible]

QY	161	PI\$W\$MG\$SDMTFTVC\$ARNPVS\$R\$N\$SS\$PL\$ARKL\$CG\$AAD\$DDP\$SS\$MVL\$CLL\$V\$PLL\$LSL	240
Db	161	PI\$W\$MG\$SDMTFTVC\$ARNPVS\$R\$N\$SS\$PL\$ARKL\$CG\$AAD\$DDP\$SS\$MVL\$CLL\$V\$PLL\$LSL	240
QY	241	FVL\$GFL\$MFL\$PK\$ERO\$EY\$IE\$E\$K\$K\$R\$VDIC\$E\$T\$P\$NIC\$PH\$G\$E\$N\$T\$E\$Y\$D\$T\$P\$H\$N\$R\$T\$IL\$K\$ED\$PA	3000
Db	241	FVL\$GFL\$MFL\$PK\$ERO\$EY\$IE\$E\$K\$K\$R\$VDIC\$E\$T\$P\$NIC\$PH\$G\$E\$N\$T\$E\$Y\$D\$T\$P\$H\$N\$R\$T\$IL\$K\$ED\$PA	3000
QY	301	NTV\$V\$T\$VEI\$PK\$K\$EN\$PH\$SL\$LT\$MP\$D\$T\$P\$RL\$F\$AY\$EN\$VI	335
Db	301	NTV\$V\$T\$VEI\$PK\$K\$EN\$PH\$SL\$LT\$MP\$D\$T\$P\$RL\$F\$AY\$EN\$VI	335
RESULT 3			
AA44603			
ID	AA44609	standard; protein; 335 AA.	
AC	AA44609;		
DT	07-APR-2000	(first entry)	
DE	Human myocardium protein-7.		
KM	Human myocardium protein-7; MP-7; congestive heart failure;		
KM	cardiovascular disorder; cardiomyopathy; hypertension; atherosclerosis;		
KM	coronary artery spasm; coronary artery disease; cell-cell interaction;		
KM	hypertensive; cardiac; screening assay.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
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FT		24..335	
FT		/note= "mature protein"	
FT	Domain	34..107	
FT		/note= "First extracellular Ig-like domain"	
FT	Domain	144..197	
FT		/note= "Second extracellular Ig-like domain"	
FT	Domain	226..250	
FT		/label= transmembrane_domain	
FT	Domain	229..250	
FT		/label= Leucine_zipper_domain	
FT	Domain	250..335	
FT		/label= Cytoplasmic_domain	
PN	WO9967387-A2.		
XX			
PD	29-DEC-1999.		
XX			
PF	24-JUN-1999;	99WO-US014307.	
XX			
PR	25-JUN-1998;	98US-0090579P.	
PR	29-SEP-1998;	98US-00163284.	
PR	02-MAR-1999;	99US-00261759.	
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Khadadoust M;		
XX			
DR	WPI; 2000-136984/12.		
DR	N-P\$DB; AA249571.		
XX			
PT	Novel myocardium protein-7 polynucleotides, used to modulate a variety of		
PT	cellular processes.		
XX			
PS	Claim 2; Fig 2; 16pp; English.		
CC	The present sequence is myocardium protein-7 (MP-7). MP-7 is used to		
CC	modulate a variety of cellular processes e.g. modulating the activity of		
CC	proteins involved in cardiovascular disorders like congestive heart		
CC	failure or cardiomyopathy. Diseases which can be treated include		
CC	hypertension, atherosclerosis, coronary artery spasm, and coronary artery		

CC disease. MP-7 proteins may also be used for cellular regulation of immune  
 CC cell types, cell cycle, differentiation of multipotent cells, and  
 CC modulation of cell-cell interactions. MP-7 may also be used in screening  
 CC assays to identify agonists and antagonists and to raise antibodies  
 XX  
 SQ Sequence 335 AA;

Query Match 100.0%; Score 1772; DB 3; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 6,9e-163;  
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILMQLTGSAAAGPVKEIVSGAVTFPLKSKVKQVDSIVTNTPTPL 60  
 1 MAGSPCTCLTIYILMQLTGSAAAGPVKEIVSGAVTFPLKSKVKQVDSIVTNTPTPL 60  
 DB 1 MAGSPCTCLTIYILMQLTGSAAAGPVKEIVSGAVTFPLKSKVKQVDSIVTNTPTPL 60  
 QY 61 VTIOPEGGTTIYQNRNRERVDPPDGGYSIKLSKLNKNDGSIYVGIYSSSLQOPSTQEX 120  
 61 VTIOPEGGTTIYQNRNRERVDPPDGGYSIKLSKLNKNDGSIYVGIYSSSLQOPSTQEX 120  
 DB 61 VTIOPEGGTTIYQNRNRERVDPPDGGYSIKLSKLNKNDGSIYVGIYSSSLQOPSTQEX 120  
 QY 121 VLVHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180  
 121 VLVHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180  
 DB 121 VLVHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180  
 QY 181 PISMWGESDMTEICVARNPVSRRNFSSPIIARLCEGAADDPSSMWLCLLIVPLLSL 240  
 181 PISMWGESDMTEICVARNPVSRRNFSSPIIARLCEGAADDPSSMWLCLLIVPLLSL 240  
 DB 181 PISMWGESDMTEICVARNPVSRRNFSSPIIARLCEGAADDPSSMWLCLLIVPLLSL 240  
 QY 241 FVLGLFLWFLKREOREBYIEKKRVDCRETPNICPHSGENTEDTIPHTNRTILKEDPA 300  
 241 FVLGLFLWFLKREOREBYIEKKRVDCRETPNICPHSGENTEDTIPHTNRTILKEDPA 300  
 DB 241 FVLGLFLWFLKREOREBYIEKKRVDCRETPNICPHSGENTEDTIPHTNRTILKEDPA 300  
 QY 301 NTYYSTVEIPKKNENPHSLTMDPTPLFAVENVI 335  
 301 NTYYSTVEIPKKNENPHSLTMDPTPLFAVENVI 335  
 DB 301 NTYYSTVEIPKKNENPHSLTMDPTPLFAVENVI 335

## RESULT 4

AAU29119  
 ID AAU29119 standard; protein; 335 AA.

XX AAU29119;  
 AC  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human PRO polypeptide sequence #96.  
 XX  
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WQ200168848-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US006520.  
 XX  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 06-MAR-2000; 2000US-0186568P.  
 PR 14-MAR-2000; 2000US-0189320P.  
 PR 14-MAR-2000; 2000US-0189328P.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 21-MAR-2000; 2000US-0190828P.  
 PR 21-MAR-2000; 2000US-0191007P.  
 PR 21-MAR-2000; 2000US-0191048P.  
 PR 21-MAR-2000; 2000US-0191314P.  
 PR 28-MAR-2000; 2000US-0192655P.  
 PR 29-MAR-2000; 2000US-0193032P.  
 PR 29-MAR-2000; 2000US-0193053P.

PR 30-MAR-2000; 2000WO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194647P.  
 PR 11-APR-2000; 2000US-0195975P.  
 PR 11-APR-2000; 2000US-0196000P.  
 PR 11-APR-2000; 2000US-0196187P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-01966820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199554P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.

(GETH ) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,  
 Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI, 2001-602746/68.

N-PSDB; AAS46020.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 presence of tumors, such as prostate and breast tumors, in mammals and to  
 screen for modulators of the compounds.

Claim 11; Fig 192; 774bp; English.

Sequences AAU29024-AAU29128 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX  
 XX  
 SQ Sequence 335 AA;

Query Match 100.0%; Score 1772; DB 4; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 6,9e-163;  
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILMQLTGSAAAGPVKEIVSGAVTFPLKSKVKQVDSIVTNTPTPL 60  
 1 MAGSPCTCLTIYILMQLTGSAAAGPVKEIVSGAVTFPLKSKVKQVDSIVTNTPTPL 60  
 DB 1 MAGSPCTCLTIYILMQLTGSAAAGPVKEIVSGAVTFPLKSKVKQVDSIVTNTPTPL 60  
 QY 61 VTIOPEGGTTIYQNRNRERVDPPDGGYSIKLSKLNKNDGSIYVGIYSSSLQOPSTQEX 120  
 61 VTIOPEGGTTIYQNRNRERVDPPDGGYSIKLSKLNKNDGSIYVGIYSSSLQOPSTQEX 120  
 DB 61 VTIOPEGGTTIYQNRNRERVDPPDGGYSIKLSKLNKNDGSIYVGIYSSSLQOPSTQEX 120  
 QY 121 VLVHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180  
 121 VLVHVEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180

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Db      121 VLAHYEHLSPKRVYTMGLQSNKNGTCVTNLTCMEHGEEDVITYTKALQGANESHNGSL 180
QY      181 PISWRGSEDMTFICVARNPVSRNFSPIIARKLCEGAADDPSSMVLCLLVPLLSL 240
Db      181 PISWRGSEDMTFICVARNPVSRNFSPIIARKLCEGAADDPSSMVLCLLVPLLSL 240
QY      241 FVLGLFLWFLKREEROEYIEKKRVDCRETENICPHSGENTYDTIPTHNTIILKEDPA 300
Db      241 FVLGLFLWFLKREEROEYIEKKRVDCRETENICPHSGENTYDTIPTHNTIILKEDPA 300
QY      301 NTVYSTVEIPKKNENPHSLTMPDTPRLFAVENVI 335
Db      301 NTVYSTVEIPKKNENPHSLTMPDTPRLFAVENVI 335

RESULT 5
AAB87548
ID      AAB87548 standard; protein; 335 AA.
AC      AAB87548;
XX      15-MAY-2001 (first entry)
DT      15-MAY-2001 (first entry)
XX      Human PRO1138.
XX      Human; PRO protein; mapping.
OS      Homo sapiens.
XX      WO200116318-A2.
XX      08-MAR-2001.
PD      24-AUG-2000; 2000WO-US023328.
XX      01-SEP-1999; 99WO-US020111.
XX      15-SEP-1999; 99WO-US021090.
XX      07-DEC-1999; 99US-016949SP.
XX      09-DEC-1999; 99US-0170262P.
XX      11-JAN-2000; 2000US-0175481P.
XX      18-FEB-2000; 2000WO-US004341.
XX      18-FEB-2000; 2000WO-US004342.
XX      22-FEB-2000; 2000WO-US004414.
XX      01-MAR-2000; 2000WO-US005601.
XX      03-MAR-2000; 2000US-0187202P.
XX      21-MAR-2000; 2000US-0191007P.
XX      30-MAR-2000; 2000WO-US008439.
XX      25-APR-2000; 2000US-0199397P.
XX      22-MAY-2000; 2000WO-US014042.
XX      05-JUN-2000; 2000US-0209832P.
XX      (GETH ) GENENTECH INC.
XX      PA
XX      Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX      PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX      DR WPI; 2001-183260/18.
XX      N-PSDB; AAF92080.
XX      Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
XX      PT biology, including use as hybridization probes, and in chromosome and
XX      FT gene mapping.
XX      Claim 12; Fig 46; 278bp; English.
XX      PS
XX      CC The present sequence is a human PRO polypeptide (secreted and
XX      CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
XX      CC anti-PRO antibodies are useful for preparation of a medicament useful in
XX      CC the treatment of a condition which is responsive to the PRO protein,
XX      CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
XX      CC employed as molecular weight markers for protein electrophoresis. The PRO
XX      CC coding sequence has applications in molecular biology, including use as
XX      CC hybridisation probes, and in chromosome and gene mapping

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XX      SQ      sequence 335 AA;
XX      Query Match      100.0%; Score 1772; DB 4; Length 335;
XX      Best Local Similarity 100.0%; Pred. No. 6.9e-163;
XX      Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MAGSPCTCLLIYIIMQLTGSAAAGPVKELVSGAVTFPLSKYKQVDSIWTENTTPL 60
Db      1 MAGSPCTCLLIYIIMQLTGSAAAGPVKELVSGAVTFPLSKYKQVDSIWTENTTPL 60
QY      61 VTIOPEGGIIYTONRNERVDFFPDGYSLKSLSKLKKNDSGIYYGIYSSIQDPSTORY 120
Db      61 VTIOPEGGIIYTONRNERVDFFPDGYSLKSLSKLKKNDSGIYYGIYSSIQDPSTORY 120
QY      121 VLAHYEHLSPKRVYTMGLQSNKNGTCVTNLTCMEHGEEDVITYTKALQGANESHNGSL 180
Db      121 VLAHYEHLSPKRVYTMGLQSNKNGTCVTNLTCMEHGEEDVITYTKALQGANESHNGSL 180
QY      181 PISWRGSEDMTFICVARNPVSRNFSPIIARKLCEGAADDPSSMVLCLLVPLLSL 240
Db      181 PISWRGSEDMTFICVARNPVSRNFSPIIARKLCEGAADDPSSMVLCLLVPLLSL 240
QY      241 FVLGLFLWFLKREEROEYIEKKRVDCRETENICPHSGENTYDTIPTHNTIILKEDPA 300
Db      241 FVLGLFLWFLKREEROEYIEKKRVDCRETENICPHSGENTYDTIPTHNTIILKEDPA 300
QY      301 NTVYSTVEIPKKNENPHSLTMPDTPRLFAVENVI 335
Db      301 NTVYSTVEIPKKNENPHSLTMPDTPRLFAVENVI 335

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RESULT 6
AAB47321
ID      AAB47321 standard; protein; 335 AA.
XX      AAB47321;
XX      29-ALG-2001 (first entry)
XX      APEX-1.
XX      Antigen presenting cell expression protein; APEX-1; APEX-2; APEX-3;
XX      KW extracellular domain; immunoglobulin-like domain; Ig-like structure;
XX      KW N-glycosylation site; transmembrane domain; cytoplasmic domain;
XX      KW SH2-binding motif; asthma; arteriosclerosis; AIDS; cirrhosis;
XX      KW Crohn's disease; atopic dermatitis; autoimmune anemia; bursitis;
XX      KW cholecystitis; diabetes mellitus; emphysema; atrophic gastritis;
XX      KW inflammatory bowel disease; multiple sclerosis; myasthenia gravis;
XX      KW myocardial inflammation; pericardial inflammation; osteoarthritis;
XX      KW osteoporosis; psoriasis; Reiter's syndrome; rheumatoid arthritis;
XX      KW inflammation; cancer; autoimmune disease; graft rejection;
XX      KW graft versus host disease; systemic lupus erythematosus.
XX      KW
XX      OS      Homo sapiens.
XX      XX
XX      FH      Key      Location/Qualifiers
XX      FT      Peptide      1..22
XX      FT      Protein      /label= Signal peptide
XX      FT      /label= Signal peptide
XX      FT      Domain      23..335
XX      FT      /label= Mature APEX-1
XX      FT      /label= Mature APEX-1
XX      FT      /label= Mature APEX-1
XX      PN      WO200146260-A2.
XX      XX
XX      PD      28-JUN-2001.
XX      XX
XX      PF      22-DEC-2000; 2000WO-US034963.
XX      XX
XX      PR      23-DEC-1999; 99US-0172025P.
XX      XX
XX      PA      (BRIM ) ERISTOL-MYERS SQUIBB CO.

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XX Starting GC, Finger J;  
 PI MPI; 2001-418044/44.  
 DR N-PSDB; AAC86114.  
 XX  
 PT Novel Antigen presenting cell expression protein useful for treating  
 PT asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's  
 PT disease and atopic dermatitis.  
 XX  
 PS Claim 3; Fig 2; 112pp; English.  
 XX  
 CC The sequences given in AAB47321-23 represent antigen presenting cell  
 CC expression (APEX)-1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2  
 CC comprise an extracellular domain having one immunoglobulin (Ig)-like  
 CC structure and N-glycosylation site, a transmembrane domain, and a  
 CC cytoplasmic domain having at least one SH2-binding motif. APEX proteins  
 CC and antibodies are useful in the study, diagnosis, prevention and  
 CC treatment of disease associated with the presence of an APEX protein  
 CC e.g., asthma, arteriosclerosis, AIDS, cirrhosis, Crohn's disease, atopic  
 CC dermatitis, autoimmune anaemia, bursitis, cholecystitis, diabetes  
 CC mellitus, emphysema, atrophic gastritis, inflammatory bowel disease,  
 CC multiple sclerosis, myasthenia gravis, myocardial or pericardial  
 CC inflammation, osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome,  
 CC rheumatoid arthritis, inflammation, cancer, immune disorders, autoimmune  
 CC diseases, graft rejections, graft versus host reaction and systemic lupus  
 CC erythematosus. APEX proteins are useful as diagnostic and/or prognostic  
 CC markers on APCs or APEX expressing cells, the ability to elicit the  
 CC generation of antibodies and as targets for various therapeutic  
 CC modalities. APEX proteins are also useful for identifying and isolating  
 CC ligand that bind APEX  
 XX  
 SQ Sequence 335 AA;

Query Match 100.0%; Score 1772; DB 4; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-163;  
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPTCLTITVITLQNGAASGPVKEVSGAVTFLKRVQVDSIVTFTPTPL 60  
 DB 1 MASPTCLTITVITLQNGAASGPVKEVSGAVTFLKRVQVDSIVTFTPTPL 60  
 QY 61 VTIOPEGGTTIVQNNRREVDPPDGGYSKLKSKKNDGIVYVGIYSSLSQGPSTOEY 120  
 DB 61 VTIOPEGGTTIVQNNRREVDPPDGGYSKLKSKKNDGIVYVGIYSSLSQGPSTOEY 120  
 QY 121 VLVHYEHLSPKRVYTMGLQSNKNGCTVNTLTCMEHGEDEVITYMKALGQANSHNGSIL 180  
 DB 121 VLVHYEHLSPKRVYTMGLQSNKNGCTVNTLTCMEHGEDEVITYMKALGQANSHNGSIL 180  
 QY 181 PISWRNGESDMTFCVARNVSRNRPSPILARLCEGAADPPSSNWLCLLVPLLSL 240  
 DB 181 PISWRNGESDMTFCVARNVSRNRPSPILARLCEGAADPPSSNWLCLLVPLLSL 240  
 QY 241 FVLGLFLMFLKRESEYIEKRVDCRETPNICPSGENTGYDTPHTNTITLKEDPA 300  
 DB 241 FVLGLFLMFLKRESEYIEKRVDCRETPNICPSGENTGYDTPHTNTITLKEDPA 300  
 QY 301 NTYVSTVEIPKQENPHSLTTPDTPRLFAVENVI 335  
 DB 301 NTYVSTVEIPKQENPHSLTTPDTPRLFAVENVI 335

RESULT 7  
 AAB65224 standard; protein; 335 AA.  
 ID AAB65224  
 AC AAB65224;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human PRO1138 (UN0576) protein sequence SEQ ID NO:253.  
 XX

KM Human; secreted and transmembrane protein; PRO; cytosolic; cell death;  
 KM cancer; chromosomal mapping; gene mapping; tissue typing;  
 KM diagnostic assay.  
 OS Homo sapiens.  
 XX  
 OS  
 PN WO200073454-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 XX 30-MAR-2000; 2000WO-US008439.  
 XX

02-JUN-1999; 99WO-US012252.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 07-JUL-1999; 99US-0143048P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 17-AUG-1999; 99US-0149396P.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 08-OCT-1999; 99US-0158663P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US003341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 PI Ashkenazi AJ, Baker KP, Botstein D, Denoyers L, Eaton DJ,  
 PI Ferreira N, Fong S, Gether H, Gerlitsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 XX  
 DR MPI; 2001-032160/04.  
 DR N-PSDB; AAF44186.  
 XX  
 PT PRO polynucleotides used to produce polypeptides used to target bioactive  
 PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
 PT to cause targeted cell death.  
 XX  
 PS Claim 12; Fig 171; 935pp; English.  
 XX

The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
 CC be used for targeted delivery of bioactive molecules, such as toxins,  
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and  
 CC DNA. They may also be used to produce transgenic animals which are used  
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide  
 CC and protein sequence can be used for tissue typing and in treating  
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF4470 to  
 CC AAF4470 represent PCR primers and hybridisation probes used in the  
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to  
 CC AAB65300 represent human PRO polynucleotide and protein sequences given  
 CC in the exemplification of the present invention

Query Match 100.0%; Score 1772; DB 4; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-163;





CC acide encoding the proteins, vectors, host cells, fusion proteins and  
CC antibodies which specifically bind to the proteins. The proteins are  
CC useful for detecting a polypeptide designated as A, B, C or D in a sample  
CC suspected of containing an A, B, C or D polypeptide, by contacting the  
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)  
CC and determining the formation of an A/E, B/F, C/G, D/H or E/I polypeptide  
CC conjugate in the sample, where the formation of the conjugate is  
CC indicative of the presence of an A, B, C or D polypeptide in the sample,  
CC where A is a PRO1072 polypeptide, B is a PRO20110 polypeptide, C is a  
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801  
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a  
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises  
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,  
CC H or I polypeptide is labeled with a detectable label or is attached to a  
CC solid support. The proteins are useful for linking a bioactive molecule  
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,  
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.  
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,  
CC or I, or antibodies against them are useful for modulating a biological  
CC activity of a cell expressing a polypeptide designated as A, B, C or D or  
CC E, F, G, H, or I. The cell is killed. The proteins are useful for  
CC identifying agonists or antagonists, for the preparation of a medicament  
CC useful in the treatment of a condition which is responsive to the  
CC proteins, as molecular weight markers for protein electrophoresis  
CC purposes, and as therapeutic agents for treating sports-related joint  
CC problems, articular cartilage defects, osteoarthritis or rheumatoid  
CC arthritis. Nucleic acids encoding the proteins are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation  
CC of anti-sense RNA and DNA, for the preparation of the proteins, to  
CC generate transgenic or knockout animals which are useful in the  
CC development and screening of therapeutic useful reagents, for chromosome  
CC identification, and in gene therapy. The antibody is useful as a  
CC therapeutic agent, in a diagnostic assay and for affinity purification of  
CC the protein from recombinant cell culture natural sources. The present  
CC sequence represents a novel secreted or transmembrane protein of the  
XX invention

XX  
XX  
SQ Sequence 335 AA.

Query Match

100.0%; Score 1772; DB 5; Length 335;

Best Local Similarity 100.0%; Pred. No. 6,9e-163;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSPTCLTIYILMOLTGSAAGPVKELVGSNGATPPLKRVQVDSIVWTFMTPL 60  
DB 1 MASSPTCLTIYILMOLTGSAAGPVKELVGSNGATPPLKRVQVDSIVWTFMTPL 60  
QY 61 VTIOPEGGTTIYONRRREKRVDPDGGYSILKSLKKNDSGIYVVGYSLSLOOPTOEY 120  
DB 61 VTIOPEGGTTIYONRRREKRVDPDGGYSILKSLKKNDSGIYVVGYSLSLOOPTOEY 120  
QY 121 VLVHYEHLSPKVTMGISQNKNGTCVNTNLCCMEHGEDVITYWKALGOANESHGNSIL 180  
DB 121 VLVHYEHLSPKVTMGISQNKNGTCVNTNLCCMEHGEDVITYWKALGOANESHGNSIL 180  
QY 181 PISMRGESMTPTICVARNVSRNFSPIIARLCEBAADPPSSWMLCLLVPLLSL 240  
DB 181 PISMRGESMTPTICVARNVSRNFSPIIARLCEBAADPPSSWMLCLLVPLLSL 240  
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DB 241 FVVLGLFVLPFKREBOEYIEKKRVDCRETPNICPSGNTXEDTIPHTNRITLKEDPA 300  
QY 301 NTYVSTVEIPKKNENPHSLLTMPDTPRLFAVENVI 335  
DB 301 NTYVSTVEIPKKNENPHSLLTMPDTPRLFAVENVI 335

RESULT 9  
ABUS8495  
ID ABUS8495 standard; protein; 335 AA.  
XX  
AC ABUS8495;

XX 15-APR-2003 (first entry)  
DT Human PRO polypeptide #96.  
XX  
XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
XX dog; cat; cow; horse; sheep; pig; goat; rabbit; ADAPT;  
XX antibody-dependent enzyme mediated produg therapy.  
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XX Homo sapiens.  
PN US2003027272-A1.  
XX  
PD 06-FEB-2003.  
XX  
XX 21-UTN-2002; 2002US-00176492.  
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Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 6.9e-163;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTYIIMQLGSAAGPVKELVGSVGAVTFPLSKSKKQVDSIWMFNTPL 60  
DB : MAGSPTCLTYIIMQLGSAAGPVKELVGSVGAVTFPLSKSKKQVDSIWMFNTPL 60  
QY 61 VTIOPEGTTIIVTONRNERVDPPDGGYSLKLSKLKKNDSGIYVGISSLOQSTOEY 120  
DB 61 VTIOPEGTTIIVTONRNERVDPPDGGYSLKLSKLKKNDSGIYVGISSLOQSTOEY 120  
QY 121 VLAHYEHLSKPKVTMGLSNNKNGTCVTNLTCCMEHGEEDVIYTWALQOANESHNGSL 180  
DB 121 VLAHYEHLSKPKVTMGLSNNKNGTCVTNLTCCMEHGEEDVIYTWALQOANESHNGSL 180  
QY 181 PISWRGSDMTFFICVANPNVSRNPSPIARKLCEGAADPDSSMVLCLLVPFLSL 240  
DB 181 PISWRGSDMTFFICVANPNVSRNPSPIARKLCEGAADPDSSMVLCLLVPFLSL 240  
QY 241 FVLGLFLFWLKRROEBYIEBKRVDICRETPNICPHSGENTYDITIPIHTNRTLIKEDPA 300

Db	241	FVGLFLMFLKRRQREYIEKKRVDCRTPNICHSGSENTYDITPHNRIILKEDPA	300
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Db	301	NTVSTVEIPKKNENPHSLTMDTPRLFAVENVI	335
RESULT 10			
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DT	07-JUL-2003	(first entry)	
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DE		Novel human secreted and transmembrane protein PRO1138.	
XX			
KW		Human; secreted and transmembrane protein; PRO; gene therapy;	
KW		tumour necrosis factor-alpha release; TNF-alpha release;	
KW		chondrocyte proliferation; chondrocyte differentiation; tumour;	
KW		adrenal tumour; lung tumour; colon tumour; breast tumour;	
KW		prostate tumour; rectal tumour; cervical tumour; liver tumour.	
XX			
OS		Homo sapiens.	
XX			
PN		US2003032127-A1.	
XX			
PD		13-FEB-2003.	
XX			
PF		26-JUN-2002; 2002US-00183012.	
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PR	21-OCT-1997;	97US-0063486P.	
PR	24-OCT-1997;	97US-0063120P.	
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PR	31-OCT-1997;	97US-0063870P.	
PR	31-OCT-1997;	97US-0064103P.	
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Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 6; 9e-163;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPTCLTYITIMQTSASGPVKELVGSVGAVTPEPLSKYKQVDSIWTFTPTPL 60  
DB 1 MGSPTCLTYITIMQTSASGPVKELVGSVGAVTPEPLSKYKQVDSIWTFTPTPL 60

QY 61 VTIOPEGGIIIVTONRNRERVDPPDGYSLKLSKLKNDSGIYVGISSSLQGPSTQEX 120  
DB 61 VTIOPEGGIIIVTONRNRERVDPPDGYSLKLSKLKNDSGIYVGISSSLQGPSTQEX 120  
QY 121 VLHYTEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQOANESNGSIL 180  
DB 121 VLHYTEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQOANESNGSIL 180  
QY 181 PISMRMGSDMTFICVARNPVSRNFSPI LARKLCEGAADPPDSSMTLCLLVLPLLSL 240  
DB 181 PISMRMGSDMTFICVARNPVSRNFSPI LARKLCEGAADPPDSSMTLCLLVLPLLSL 240  
QY 241 FVLGLFLWFLKRRQEEYIEEKKRVDICRETPNICPHSGENTEXDTIPIHNRITLIKEDPA 300  
DB 241 FVLGLFLWFLKRRQEEYIEEKKRVDICRETPNICPHSGENTEXDTIPIHNRITLIKEDPA 300  
QY 301 NTIVSTVEIPKKMENPHSLTMPDTPRLFAVENYI 335  
DB 301 NTIVSTVEIPKKMENPHSLTMPDTPRLFAVENYI 335

RESULT 11  
ABU84358  
ID ABU84358 standard; protein, 335 AA.  
XX ABU84358;  
AC ABU84358;  
XX 02-ALG-2003 (first entry)  
DT Human secreted/transmembrane protein (PRO) #96.  
XX Human; secreted and transmembrane protein; PRO; TNF-alpha;  
DE tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing.  
XX Homo sapiens.  
OS US200:032112-A1.  
XX 13-FEE-2003.  
PD 21-JUN-2002; 2002US-00176756.  
XX 18-SEP-1997; 97US-0059263P.  
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PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
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PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 6,9e-163;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAGSPCTCLTLYIIMQITGSAAGPYKEIVSGAVTPEPLSKYQVDSITWTFPTPL 60  
QY 61 VTIOEGGTIIIVTONRREVRVDPDGYSLKSLKLNDSGIYVYGIYSSIQOESTORY 120  
DB 61 VTIOEGGTIIIVTONRREVRVDPDGYSLKSLKLNDSGIYVYGIYSSIQOESTORY 120  
QY 121 VHAHYEHLSPKYTMGLQSNKNGTCYTNLTCCMEHGEEDVIYTKALGOANESHNGSL 180  
DB 121 VHAHYEHLSPKYTMGLQSNKNGTCYTNLTCCMEHGEEDVIYTKALGOANESHNGSL 180  
QY 181 PLSMRGSDMTFICARNPVSRNFPSPILARKLCGADDPDSSWVLCILVPLLSL 240  
DB 181 PLSMRGSDMTFICARNPVSRNFPSPILARKLCGADDPDSSWVLCILVPLLSL 240  
QY 241 FVLGLFLMLKEEROEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300  
DB 241 FVLGLFLMLKEEROEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300  
QY 301 NNTVYSIVELPKKMNENSHLLTMDPTPLPAYENVI 335  
DB 301 NNTVYSIVELPKKMNENSHLLTMDPTPLPAYENVI 335

## RESULT 12

ABR66232  
ID ABR66232 standard; protein; 335 AA.

XX ABR66232;

DT 05-AUG-2003 (first entry)

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

XX Human; PRO; secreted protein; transmembrane protein; TNF-alpha;  
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antidiabetic; vulnerary; gene therapy.

OS Homo sapiens.

XX US2003027278-A1.

PD 06-FEB-2003.

PF 21-JUN-2002; 2002US-00176987.

XX 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
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PR 12-DEC-1997; 97US-0069425P.  
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PR 18-DEC-1997; 97US-0068017P.  
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Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 6, 9e-163; Indels 0; Gaps 0;  
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QY 61 VTIOPEGGTIIYTONRNRVRVPPDGGYSLKSLKKNDSIGIYYGIVSSIQOPESTOXY 120  
DB 61 VTIOPEGGTIIYTONRNRVRVPPDGGYSLKSLKKNDSIGIYYGIVSSIQOPESTOXY 120  
QY 121 VLVHVEHLKSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180  
121 VLVHVEHLKSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180  
DB 121 VLVHVEHLKSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180  
QY 181 PISMRWGESDMTFICVARNPVSRNFSPIIARKLCEGAADDDSSWVLLCLLVPLLSL 240  
181 PISMRWGESDMTFICVARNPVSRNFSPIIARKLCEGAADDDSSWVLLCLLVPLLSL 240  
DB 181 PISMRWGESDMTFICVARNPVSRNFSPIIARKLCEGAADDDSSWVLLCLLVPLLSL 240  
QY 241 FVLGLFLMFLKREKREVEYIEKKRVDICRETENICPHSEENYPTIPTNTTILKEDPA 300  
241 FVLGLFLMFLKREKREVEYIEKKRVDICRETENICPHSEENYPTIPTNTTILKEDPA 300  
DB 241 FVLGLFLMFLKREKREVEYIEKKRVDICRETENICPHSEENYPTIPTNTTILKEDPA 300  
QY 301 NTIVYSTVEIPKKMENPHSLLTWPDTPRLPAYENVI 335  
301 NTIVYSTVEIPKKMENPHSLLTWPDTPRLPAYENVI 335  
DB 301 NTIVYSTVEIPKKMENPHSLLTWPDTPRLPAYENVI 335

## RESULT 13

ABR65622  
ID ABR65622 standard; protein; 335 AA.

AC ABR65622;

DT 05-AUG-2003 (first entry)

DE Human secreted polypeptide PRO1138. SEQ ID NO:192.

XX Human; PRO; secreted protein; transmembrane protein;  
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
XX chondrocyte; proliferation; differentiation; cartilage disorder;  
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
XX liver; drug screening; transgenic animal; genetic analysis;  
XX antitubercular; vulnerability; gene therapy.

OS Homo sapiens.

PN US2003036159-A1.

PD 20-FEB-2003.

PF 02-JUL-2002; 2002US-00188773.

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PR	18-SEP-1997	9.705-0059263.9
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PR	17-OCT-1997	9.705-0062250.9
PR	21-OCT-1997	9.705-0063486.9
PR	24-OCT-1997	9.705-0063120.9
PR	24-OCT-1997	9.705-0063121.9
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PR	12-DEC-1997	9.705-0069425.9
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PR	10-JUN-1998	9.705-0088722.9

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PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
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PR 01-OCT-1998; 98US-0102684P.  
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Query Match 100.0%; Score 1772; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 6,9e-163;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTLTLYIMOLTGSAAGPYKELVSGAVTFPLKSKVQVDSIVWTFNTTPL 60  
DB 1 MAGSPCTLTLYIMOLTGSAAGPYKELVSGAVTFPLKSKVQVDSIVWTFNTTPL 60  
QY 61 VTIQPGGTTIVTQNNRERVPDGGYSIKLSKLNKNDGIIYVGIIYSSSLQOPSTOEY 120  
DB 61 VTIQPGGTTIVTQNNRERVPDGGYSIKLSKLNKNDGIIYVGIIYSSSLQOPSTOEY 120  
QY 121 VLVHYHLSKPKYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYWKALGQANSHSGSL 180  
DB 121 VLVHYHLSKPKYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYWKALGQANSHSGSL 180  
QY 181 PISMRGESDMPTICVARNVSNFSPILARKLCEGAADDPDSSMWLCLLIVPLLSL 240  
DB 181 PISMRGESDMPTICVARNVSNFSPILARKLCEGAADDPDSSMWLCLLIVPLLSL 240  
QY 241 FVLGLFLWFLKREOREEYIEKKRVDCRETPNICPSGENTETDTPHTNRTILKEDPA 300  
DB 241 FVLGLFLWFLKREOREEYIEKKRVDCRETPNICPSGENTETDTPHTNRTILKEDPA 300  
QY 301 NTYVSTVEIPKKENPHSLTMDPTPLPAYENV 335  
DB 301 NTYVSTVEIPKKENPHSLTMDPTPLPAYENV 335

## RESULT 14

ABU99562 standard; protein; 335 AA.

XX ABU99562;  
XX  
XX  
XX 09-AUG-2003 (first entry)  
XX  
XX Human secreted/transmembrane protein (PRO) #96.  
DE Human secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing.

XX OS Homo sapiens.  
XX EN US2003040070-A1.  
XX  
XX 27-FEB-2003.  
PF 27-JUN-2002; 2002US-00184627.  
XX 18-SEP-1997; 97US-0059263P.  
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Query Match 100.0%; Score 1772; DB 6; Length 335;  
Beet Local Similarity 100.0%; Pred. No. 6; 9e-163;  
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DB 121 VLAHYEHLKSKPVTKGLQSNKNGTCVTNLTCMEHGEEDVIYTMKALQOANESHNGSIL 180  
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KW horse; cow; cat; sheep; pig; goat; rabbit; ADAPT;  
KM antibody-dependent enzyme mediated prodrug therapy.  
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Search completed: August 18, 2004, 16:07:18  
Job time : 57 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: August 18, 2004, 15:58:14 ; Search time 19 Seconds

(Without alignments)  
910.247 Million cell updates/sec

Title: US-10-063-551-46

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%

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Listing first 700 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	362.5	20.5	329	4 US-09-149-476-483	Sequence 483, App
2	186	10.5	343	1 US-08-348-792-10	Sequence 10, App1
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7	182.5	10.3	335	2 US-08-462-738-2	Sequence 2, App1
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9	182.5	10.3	335	4 US-08-880-875-2	Sequence 2, App1
10	182.5	10.3	335	4 US-09-369-248A-3	Sequence 2, App1
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29	140.5	7.9	143	4 US-09-227-357-192	Sequence 192, App
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83	96	5.4	526	4 US-09-910-174B-9	Sequence 9, App1
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87	95.5	5.4	771	4 US-09-312-157-8	Sequence 8, App1
88	93.5	5.3	299	3 US-09-188-930-189	Sequence 189, App
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90	93	5.2	316	4 US-09-910-174B-24	Sequence 24, App1
91	93	5.2	316	4 US-09-620-461-24	Sequence 24, App1
92	92.5	5.2	561	3 US-09-192-545-2	Sequence 2, App1
93	92.5	5.2	299	3 US-09-188-930-331	Sequence 331, App
94	92.5	5.2	299	4 US-09-462-270-2	Sequence 2, App1
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96	92.5	5.2	299	4 US-09-312-283C-189	Sequence 189, App
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103	90.5	5.1	521	3	US-08-996-338-20	Sequence 20, Appl	176	86	4.9	1069	4	US-09-877-730-2	Sequence 2, Appl
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106	90	5.1	222	1	US-08-328-152A-8	Sequence 8, Appl	179	85.5	4.8	746	2	US-08-838-219B-6	Sequence 6, Appl
107	90	5.1	240	1	US-07-940-861-12	Sequence 12, Appl	180	85.5	4.8	746	3	US-09-233-336A-6	Sequence 6, Appl
108	90	5.1	240	1	US-08-459-512-12	Sequence 12, Appl	181	85.5	4.8	746	3	US-09-233-752A-6	Sequence 6, Appl
109	90	5.1	240	2	US-08-459-657-12	Sequence 12, Appl	182	85.5	4.8	746	3	US-09-402-036-6	Sequence 6, Appl
110	90	5.1	240	2	US-08-460-132-12	Sequence 12, Appl	183	85.5	4.8	746	4	US-09-904-226-6	Sequence 6, Appl
111	90	5.1	240	3	US-08-466-465-4	Sequence 4, Appl	184	85.5	4.8	789	1	US-08-471-033-29	Sequence 29, Appl
112	90	5.1	240	5	PCT-US92-02050-12	Sequence 12, Appl	185	85.5	4.8	789	1	US-08-471-033-32	Sequence 32, Appl
113	90	5.1	240	6	5185441-36	Patent No. 5185441	186	85.5	4.8	789	2	US-08-471-044-29	Sequence 29, Appl
114	90	5.1	240	6	5223394-4	Patent No. 5223394	187	85.5	4.8	789	2	US-08-471-044-32	Sequence 32, Appl
115	90	5.1	240	6	5223394-6	Patent No. 5223394	188	85.5	4.8	789	2	US-08-463-483A-29	Sequence 29, Appl
116	90	5.1	250	1	US-07-940-861-10	Sequence 10, Appl	189	85.5	4.8	789	2	US-08-463-483A-32	Sequence 32, Appl
117	90	5.1	250	1	US-08-459-512-10	Sequence 10, Appl	190	85.5	4.8	789	2	US-08-471-046A-29	Sequence 29, Appl
118	90	5.1	250	2	US-08-459-657-10	Sequence 10, Appl	191	85.5	4.8	789	2	US-08-471-046A-32	Sequence 32, Appl
119	90	5.1	250	2	US-08-460-132-10	Sequence 10, Appl	192	85.5	4.8	789	2	US-08-470-566B-29	Sequence 29, Appl
120	90	5.1	250	3	US-08-466-465-2	Sequence 2, Appl	193	85.5	4.8	789	2	US-08-470-566B-32	Sequence 32, Appl
121	90	5.1	250	5	PCT-US92-02050-10	Sequence 10, Appl	194	85.5	4.8	789	2	US-08-838-219B-2	Sequence 2, Appl
122	90	5.1	250	6	5223394-1	Patent No. 5223394	195	85.5	4.8	789	2	US-08-838-219B-4	Sequence 4, Appl
123	90	5.1	419	6	5169835-2	Patent No. 5169835	196	85.5	4.8	789	2	US-08-469-334-29	Sequence 29, Appl
124	90	5.1	541	1	US-08-604-333-2	Sequence 2, Appl	197	85.5	4.8	789	2	US-08-469-334-32	Sequence 32, Appl
125	90	5.1	541	1	US-09-110-618-2	Sequence 2, Appl	198	85.5	4.8	789	3	US-09-300-529-29	Sequence 29, Appl
126	90	5.1	541	4	US-09-173-151A-28	Sequence 28, Appl	199	85.5	4.8	789	3	US-09-300-529-32	Sequence 32, Appl
127	90	5.1	541	4	US-09-578-178-2	Sequence 2, Appl	200	85.5	4.8	789	3	US-09-233-336A-2	Sequence 2, Appl
128	90	5.1	541	4	US-09-578-178-2	Sequence 2, Appl	201	85.5	4.8	789	3	US-09-233-336A-4	Sequence 4, Appl
129	90	5.1	541	4	US-09-621-502-4	Sequence 4, Appl	202	85.5	4.8	789	3	US-09-233-752A-2	Sequence 2, Appl
130	89.5	5.1	423	4	US-09-181-339-9	Sequence 9, Appl	203	85.5	4.8	789	3	US-09-233-752A-4	Sequence 4, Appl
131	89	5.0	303	4	US-09-651-200-23	Sequence 23, Appl	204	85.5	4.8	789	3	US-09-402-036-2	Sequence 2, Appl
132	89	5.0	309	2	US-08-456-104-4	Sequence 4, Appl	205	85.5	4.8	789	3	US-09-402-036-4	Sequence 4, Appl
133	89	5.0	309	3	US-08-479-744A-23	Sequence 23, Appl	206	85.5	4.8	789	4	US-09-002-285-78	Sequence 78, Appl
134	89	5.0	309	3	US-08-280-757B-23	Sequence 23, Appl	207	85.5	4.8	789	4	US-09-002-285-80	Sequence 80, Appl
135	89	5.0	309	3	US-08-205-697A-21	Sequence 21, Appl	208	85.5	4.8	789	4	US-09-002-285-94	Sequence 94, Appl
136	89	5.0	309	3	US-08-702-525-21	Sequence 21, Appl	209	85.5	4.8	789	4	US-09-002-285-100	Sequence 100, App
137	89	5.0	309	4	US-09-651-200-22	Sequence 22, Appl	210	85.5	4.8	789	4	US-09-904-226-2	Sequence 2, Appl
138	89	5.0	309	4	US-09-667-135-33	Sequence 33, Appl	211	85.5	4.8	789	4	US-09-904-226-4	Sequence 4, Appl
139	89	5.0	309	4	US-09-425-762-23	Sequence 23, Appl	212	85.5	4.8	789	4	US-09-589-477-78	Sequence 78, Appl
140	89	5.0	309	4	US-09-837-867A-21	Sequence 21, Appl	213	85.5	4.8	789	4	US-09-589-477-80	Sequence 80, Appl
141	89	5.0	309	5	PCT-US95-02576-21	Sequence 21, Appl	214	85.5	4.8	789	4	US-09-589-477-94	Sequence 94, Appl
142	89	5.0	314	3	US-08-205-697A-13	Sequence 13, Appl	215	85.5	4.8	789	4	US-09-589-477-100	Sequence 100, App
143	89	5.0	314	3	US-08-702-525-13	Sequence 13, Appl	216	85.5	4.8	790	3	US-08-976-780-8	Sequence 8, Appl
144	89	5.0	314	4	US-09-837-867A-13	Sequence 13, Appl	217	85.5	4.8	790	3	US-09-073-898-8	Sequence 8, Appl
145	89	5.0	314	5	PCT-US95-02576-13	Sequence 13, Appl	218	85.5	4.8	790	4	US-09-312-106-2	Sequence 2, Appl
146	89	5.0	821	1	US-09-422-869-24	Sequence 24, Appl	219	85.5	4.8	790	4	US-09-350-351A-8	Sequence 8, Appl
147	88.5	5.0	611	2	US-08-752-307B-10	Sequence 10, Appl	220	85.5	4.8	2491	4	US-09-207-353-1	Sequence 1, Appl
148	88.5	5.0	611	4	US-09-707-802-10	Sequence 10, Appl	221	85	4.8	512	4	US-08-999-689A-7	Sequence 7, Appl
149	88.5	5.0	611	4	US-09-991-326-10	Sequence 10, Appl	222	85	4.8	757	3	US-08-434-000A-6	Sequence 6, Appl
150	88	5.0	639	1	US-09-651-200-19	Sequence 19, Appl	223	85	4.8	757	4	US-09-312-157-6	Sequence 6, Appl
151	88	5.0	639	1	US-08-348-006B-7	Sequence 7, Appl	224	85	4.8	821	4	US-09-622-880B-15	Sequence 15, Appl
152	88	5.0	699	2	US-08-800-825A-7	Sequence 7, Appl	225	85	4.8	303	3	US-08-985-950-2	Sequence 2, Appl
153	88	5.0	699	3	US-09-158-657-7	Sequence 7, Appl	226	34.5	4.8	303	4	US-09-546-049-2	Sequence 2, Appl
154	87.5	4.9	325	4	US-09-651-200-20	Sequence 20, Appl	227	84	4.7	339	4	US-09-719-243-2	Sequence 2, Appl
155	87.5	4.9	769	3	US-08-434-000A-10	Sequence 10, Appl	228	84	4.7	358	4	US-09-719-243-3	Sequence 3, Appl
156	87.5	4.9	769	4	US-09-312-157-10	Sequence 10, Appl	229	84	4.7	668	1	US-08-530-950-13	Sequence 13, Appl
157	87	4.9	87	4	US-09-336-643A-6	Sequence 6, Appl	230	84	4.7	668	3	US-09-149-879-13	Sequence 13, Appl
158	87	4.9	491	4	US-09-181-339-7	Sequence 7, Appl	231	84	4.7	668	4	US-09-057-009-13	Sequence 13, Appl
159	87	4.9	582	4	US-09-702-457-334	Sequence 334, App	232	83.5	4.7	260	4	US-09-254-465A-23	Sequence 23, Appl
160	87	4.9	582	4	US-09-736-457-334	Sequence 334, App	233	83.5	4.7	263	4	US-09-254-465A-25	Sequence 25, Appl
161	87	4.9	582	4	US-09-614-124B-334	Sequence 334, App	234	83.5	4.7	298	4	US-09-152-060-76	Sequence 76, Appl
162	87	4.9	582	4	US-09-671-325-334	Sequence 334, App	235	83.5	4.7	312	4	US-09-254-465A-9	Sequence 9, Appl
163	87	4.9	582	4	US-09-589-184-334	Sequence 334, App	236	83.5	4.7	312	4	US-09-907-794A-64	Sequence 64, Appl
164	87	4.9	583	2	US-08-432-016-2	Sequence 2, Appl	237	83.5	4.7	312	4	US-09-907-125A-64	Sequence 64, Appl
165	87	4.9	583	2	US-08-684-594-2	Sequence 2, Appl	238	83.5	4.7	312	4	US-09-907-775A-64	Sequence 64, Appl
166	86.5	4.9	790	3	US-08-960-780-4	Sequence 4, Appl	239	83.5	4.7	318	3	US-09-068-051A-32	Sequence 32, Appl
167	86.5	4.9	790	3	US-09-073-898-4	Sequence 4, Appl	240	83.5	4.7	391	4	US-08-999-689A-8	Sequence 8, Appl
168	86.5	4.9	790	4	US-09-850-351A-4	Sequence 4, Appl	241	83.5	4.7	408	4	US-09-724-864-62	Sequence 62, Appl
169	86	4.9	302	4	US-09-877-730-14	Sequence 14, Appl	242	83.5	4.7	450	4	US-09-907-794A-320	Sequence 320, App
170	86	4.9	380	4	US-09-877-730-4	Sequence 4, Appl	243	83.5	4.7	450	4	US-09-905-125A-120	Sequence 120, App
171	86	4.9	826	4	US-09-877-730-16	Sequence 16, Appl	244	83.5	4.7	450	4	US-09-902-775A-320	Sequence 320, App
172	86	4.9	904	4	US-09-877-730-6	Sequence 6, Appl	245	83.5	4.7	789	4	US-09-002-285-96	Sequence 96, Appl
173	86	4.9	907	4	US-09-877-730-20	Sequence 20, Appl	246	83.5	4.7	789	4	US-09-589-477-96	Sequence 96, Appl

247	83.5	4.7	1501	2	US-08-447-464-3	Sequence 3, Appl	320	80	4.5	338	2	US-08-414-657D-43	Sequence 43, Appl
248	83.5	4.7	1501	2	US-08-716-679-3	Sequence 3, Appl	321	80	4.5	339	4	US-09-135-080-4	Sequence 4, Appl
249	83	4.7	464	1	US-09-237-468-2	Sequence 2, Appl	322	80	4.5	438	4	US-09-252-991A-23328	Sequence 23328, A
250	83	4.7	846	1	US-08-149-103-3	Sequence 3, Appl	323	80	4.5	439	4	US-09-010-147B-20	Sequence 20, Appl
251	83	4.7	846	1	US-08-451-883-3	Sequence 3, Appl	324	80	4.5	529	3	US-09-383-586-31	Sequence 31, Appl
252	83	4.7	873	1	US-08-393-734-2	Sequence 2, Appl	325	80	4.5	607	2	US-08-752-307B-12	Sequence 12, Appl
253	83	4.7	873	3	US-08-894-489-2	Sequence 2, Appl	326	80	4.5	607	4	US-09-707-802-12	Sequence 12, Appl
254	82.5	4.7	134	3	US-08-630-172-14	Sequence 14, Appl	327	80	4.5	607	4	US-09-091-326-12	Sequence 5, Appl
255	82.5	4.7	134	3	US-09-375-419-14	Sequence 14, Appl	328	80	4.5	1233	3	US-09-194-613-5	Sequence 5, Appl
256	82.5	4.7	238	4	US-09-149-476-485	Sequence 485, App	329	79.5	4.5	202	6	5169147-6	Patent No. 5169147
257	82.5	4.7	466	4	US-09-134-000C-5552	Sequence 552, Ap	330	79.5	4.5	278	4	US-09-570-367C-21	Sequence 21, Appl
258	82.5	4.7	511	4	US-09-002-285-88	Sequence 88, Appl	331	79.5	4.5	278	4	US-09-915-524-21	Sequence 21, Appl
259	82.5	4.7	511	4	US-09-589-477-88	Sequence 88, Appl	332	79.5	4.5	328	3	US-08-821-994-84	Sequence 84, Appl
260	82.5	4.7	789	4	US-09-002-285-82	Sequence 82, Appl	333	79.5	4.5	335	4	US-09-489-039A-11298	Sequence 11298, A
261	82.5	4.7	789	4	US-09-002-285-84	Sequence 84, Appl	334	79.5	4.5	374	3	US-08-821-994-68	Sequence 68, Appl
262	82.5	4.7	789	4	US-09-002-285-92	Sequence 92, Appl	335	79.5	4.5	402	4	US-09-292-097-16	Sequence 16, Appl
263	82.5	4.7	789	4	US-09-589-477-82	Sequence 82, Appl	336	79.5	4.5	643	1	US-08-471-570-6	Sequence 6, Appl
264	82.5	4.7	789	4	US-09-589-477-84	Sequence 84, Appl	337	79.5	4.5	769	1	US-08-471-570-8	Sequence 8, Appl
265	82.5	4.7	789	4	US-09-589-477-92	Sequence 92, Appl	338	79.5	4.5	859	4	US-09-708-200-7	Sequence 7, Appl
266	82.5	4.7	790	4	US-09-002-285-102	Sequence 102, App	339	79.5	4.5	859	4	US-09-788-657-16	Sequence 16, Appl
267	82.5	4.7	790	4	US-09-589-477-102	Sequence 102, App	340	78.5	4.4	393	1	US-08-429-742-2	Sequence 2, Appl
268	82	4.6	314	3	US-09-107-532A-4919	Sequence 4919, Ap	341	78.5	4.4	439	3	US-09-383-586-32	Sequence 32, Appl
269	82	4.6	449	3	US-09-118-319-7	Sequence 7, Appl	342	78.5	4.4	831	2	US-09-047-026A-4	Sequence 4, Appl
270	82	4.6	449	3	US-09-286-691-4	Sequence 4, Appl	343	78	4.4	341	1	US-08-248-628A-2	Sequence 5, Appl
271	82	4.6	449	3	US-09-687-147-4	Sequence 4, Appl	344	78	4.4	345	4	US-09-214-631-5	Sequence 5, Appl
272	82	4.6	757	4	US-09-622-880B-1	Sequence 1, Appl	345	78	4.4	624	2	US-08-642-406A-22	Sequence 22, Appl
273	82	4.6	874	2	US-08-456-647B-6	Sequence 6, Appl	346	78	4.4	624	4	US-09-199-534-22	Sequence 22, Appl
274	82	4.6	874	2	US-08-237-401A-6	Sequence 6, Appl	347	78	4.4	624	4	US-09-199-534-22	Sequence 22, Appl
275	82	4.6	880	1	US-08-445-640-10	Sequence 10, Appl	348	77.5	4.4	421	4	US-09-254-465A-2	Sequence 4, Appl
276	82	4.6	880	3	US-08-170-558-10	Sequence 10, Appl	349	77.5	4.4	477	2	US-08-432-016-3	Sequence 3, Appl
277	82	4.6	880	3	US-08-447-114-10	Sequence 10, Appl	350	77.5	4.4	477	2	US-08-684-594-3	Sequence 3, Appl
278	82	4.6	880	3	US-08-445-461-10	Sequence 10, Appl	351	77.5	4.4	650	4	US-09-310-463-2	Sequence 2, Appl
279	81.5	4.6	309	4	US-09-667-135-6	Sequence 6, Appl	352	77.5	4.4	650	4	US-08-842-248A-2	Sequence 2, Appl
280	81.5	4.6	309	4	US-09-910-174B-7	Sequence 7, Appl	353	77.5	4.4	662	1	US-08-261-304-7	Sequence 7, Appl
281	81.5	4.6	309	4	US-09-620-461-7	Sequence 7, Appl	354	77.5	4.4	735	5	PCT-US93-00031-13	Sequence 13, Appl
282	81.5	4.6	558	4	US-09-667-135-31	Sequence 31, Appl	355	77.5	4.4	736	5	PCT-US93-00031-15	Sequence 15, Appl
283	81.5	4.6	846	1	US-08-149-103-4	Sequence 4, Appl	356	77.5	4.4	739	4	US-08-482-073-6	Sequence 6, Appl
284	81.5	4.6	846	1	US-08-451-883-4	Sequence 4, Appl	357	77.5	4.4	739	5	PCT-US93-00031-9	Sequence 9, Appl
285	81	4.6	144	6	5169835-8	Patent No. 5169835	358	77.5	4.4	1312	4	US-09-554-572-26	Sequence 26, Appl
286	81	4.6	252	2	US-08-414-657D-56	Sequence 56, Appl	359	77	4.3	278	4	US-09-570-367C-2	Sequence 2, Appl
287	81	4.6	287	2	US-08-414-657D-48	Sequence 48, Appl	360	77	4.3	458	4	US-09-915-524-2	Sequence 2, Appl
288	81	4.6	304	2	US-08-414-657D-44	Sequence 44, Appl	361	77	4.3	458	4	US-09-435-956A-1	Sequence 1, Appl
289	81	4.6	308	2	US-08-414-657D-46	Sequence 46, Appl	362	77	4.3	523	3	US-08-948-564-8	Sequence 8, Appl
290	81	4.6	325	2	US-08-414-657D-2	Sequence 2, Appl	363	77	4.3	1021	4	US-08-497-025-3	Sequence 3, Appl
291	81	4.6	325	2	US-08-414-657D-41	Sequence 41, Appl	364	77	4.3	1033	4	US-09-252-991A-20611	Sequence 20611, A
292	81	4.6	335	4	US-09-135-080-2	Sequence 2, Appl	365	76.5	4.3	364	4	US-08-896-537A-3	Sequence 3, Appl
293	81	4.6	338	2	US-08-414-657D-60	Sequence 60, Appl	366	76.5	4.3	364	4	US-08-896-537A-3	Sequence 3, Appl
294	81	4.6	338	4	US-09-135-080-8	Sequence 8, Appl	367	76.5	4.3	490	4	US-09-667-135-28	Sequence 28, Appl
295	81	4.6	338	4	US-09-676-594-404	Sequence 404, App	368	76.5	4.3	589	4	US-09-866-510-12	Sequence 12, Appl
296	80.5	4.5	205	4	US-09-134-001C-4766	Sequence 4766, Ap	369	76.5	4.3	1089	1	US-08-180-195-36	Sequence 36, Appl
297	80.5	4.5	346	1	US-08-213-403-2	Sequence 2, Appl	370	76.5	4.3	1089	1	US-08-168-917-4	Sequence 4, Appl
298	80.5	4.5	346	1	US-08-458-077-2	Sequence 2, Appl	371	76.5	4.3	1089	1	US-08-477-329-36	Sequence 36, Appl
299	80.5	4.5	346	1	US-08-460-741-2	Sequence 2, Appl	372	76.5	4.3	1089	2	US-08-475-458-36	Sequence 36, Appl
300	80.5	4.5	346	1	US-08-747-240-2	Sequence 2, Appl	373	76.5	4.3	1089	2	US-08-460-510-4	Sequence 4, Appl
301	80.5	4.5	346	1	US-08-299-567-6	Sequence 6, Appl	374	76.5	4.3	1089	2	US-08-460-490-4	Sequence 4, Appl
302	80.5	4.5	346	4	US-09-039-642B-2	Sequence 2, Appl	375	76.5	4.3	1089	3	US-08-980-400-36	Sequence 36, Appl
303	80.5	4.5	650	1	US-08-121-713D-60	Sequence 60, Appl	376	76.5	4.3	1089	3	US-08-462-728-2	Sequence 2, Appl
304	80.5	4.5	650	1	US-08-835-268-60	Sequence 60, Appl	377	76.5	4.3	1089	3	US-09-583-4159A-36	Sequence 36, Appl
305	80.5	4.5	650	2	US-09-060-692-60	Sequence 60, Appl	378	76.5	4.3	1089	3	US-09-583-210-36	Sequence 36, Appl
306	80.5	4.5	650	3	US-08-833-391-60	Sequence 60, Appl	379	76.5	4.3	1089	4	US-09-583-449A-36	Sequence 36, Appl
307	80.5	4.5	650	4	US-09-060-610-60	Sequence 60, Appl	380	76.5	4.3	1089	4	US-09-435-059-36	Sequence 36, Appl
308	80.5	4.5	650	5	PCT-US94-10151A-60	Sequence 60, Appl	381	76.5	4.3	1089	4	US-08-461-917-2	Sequence 2, Appl
309	80.5	4.5	721	4	US-09-350-234-80	Sequence 20, Appl	382	76.5	4.3	1089	4	US-08-464-436-2	Sequence 2, Appl
310	80.5	4.5	721	4	US-09-603-311-20	Sequence 20, Appl	383	76.5	4.3	1089	4	US-08-464-436-2	Sequence 2, Appl
311	80.5	4.5	789	3	US-08-960-780-6	Sequence 6, Appl	384	76.5	4.3	1089	4	US-09-769-987-2	Sequence 2, Appl
312	80.5	4.5	789	3	US-09-073-898-6	Sequence 6, Appl	385	76.5	4.3	1089	4	US-09-866-510-2	Sequence 2, Appl
313	80.5	4.5	789	4	US-09-850-351A-6	Sequence 6, Appl	386	76.5	4.3	1089	4	US-09-866-510-4	Sequence 4, Appl
314	80.5	4.5	828	1	US-08-261-304-2	Sequence 2, Appl	387	76.5	4.3	1089	4	US-09-866-510-6	Sequence 6, Appl
315	80	4.5	252	2	US-08-414-657D-57	Sequence 57, Appl	388	76.5	4.3	1089	4	US-09-866-510-8	Sequence 8, Appl
316	80	4.5	287	2	US-08-414-657D-49	Sequence 49, Appl	389	76.5	4.3	1089	4	US-09-866-510-10	Sequence 10, Appl
317	80	4.5	315	2	US-08-414-657D-45	Sequence 45, Appl	390	76.5	4.3	1089	5	PCT-US92-00730-4	Sequence 4, Appl
318	80	4.5	315	2	US-08-414-657D-47	Sequence 47, Appl	391	76.5	4.3	1089	5	PCT-US92-00862-4	Sequence 4, Appl
319	80	4.5	338	2	US-08-414-657D-42	Sequence 42, Appl	392	76.5	4.3	1328	3	US-08-781-891-76	Sequence 76, Appl

393	76.5	4.3	1328	4	US-09-618-166-76	Sequence 76, Appl
394	76.5	4.3	1723	4	US-09-194-612A-31	Sequence 31, Appl
395	76.5	4.3	1745	4	US-09-800-729-89	Sequence 89, Appl
396	76	4.3	277	4	US-09-543-681A-4527	Sequence 4527, Ap
397	76	4.3	378	1	US-08-225-477B-9	Sequence 9, Appl1
398	76	4.3	378	5	PCT-US95-04353-9	Sequence 9, Appl1
399	76	4.3	330	3	US-08-961-564A-2	Sequence 2, Appl1
400	76	4.3	390	4	US-09-050-861B-2	Sequence 1, Appl1
401	76	4.3	463	3	US-09-082-310-1	Sequence 1, Appl1
402	76	4.3	463	4	US-09-575-205-1	Sequence 721, Appl
403	76	4.3	463	4	US-09-576-594-721	Sequence 18, Appl
404	76	4.3	559	1	US-08-442-542-18	Sequence 18, Appl
405	76	4.3	559	1	US-08-765-469-18	Sequence 2, Appl1
406	75.5	4.2	648	2	US-08-817-436A-2	Sequence 7, Appl1
407	75	4.2	303	4	US-09-509-347-7	Sequence 2, Appl1
408	75	4.2	512	3	US-09-356-818A-2	Sequence 10, Appl
409	75	4.2	527	4	US-09-910-174B-10	Sequence 10, Appl
410	75	4.2	527	4	US-09-620-461-10	Sequence 10, Appl
411	75	4.2	641	3	US-09-422-869-26	Sequence 26, Appl
412	75	4.2	855	4	US-09-328-352-6216	Sequence 26, Appl
413	75	4.2	1729	4	US-09-696-115B-2	Sequence 2, Appl1
414	75	4.2	2137	4	US-09-134-001C-4463	Sequence 4463, Ap
415	74.5	4.2	218	3	US-09-068-655-7	Sequence 7, Appl1
416	74.5	4.2	230	6	5169835-13	Sequence 7, Appl1
417	74.5	4.2	338	4	US-09-688-188B-152	Patent No. 5169835
418	74.5	4.2	338	4	US-09-291-417D-152	Sequence 152, App
419	74.5	4.2	373	4	US-09-688-188B-97	Sequence 97, Appl
420	74.5	4.2	373	4	US-09-291-417D-97	Sequence 97, Appl
421	74.5	4.2	374	3	US-08-821-994-67	Sequence 67, Appl
422	74.5	4.2	374	3	US-08-821-994-69	Sequence 69, Appl
423	74.5	4.2	463	2	US-08-853-659A-52	Sequence 52, Appl
424	74.5	4.2	789	4	US-09-002-285-98	Sequence 98, Appl
425	74.5	4.2	789	4	US-09-589-477-98	Sequence 2, Appl1
426	74.5	4.2	1018	1	US-08-452-052-2	Sequence 2, Appl1
427	74.5	4.2	1148	2	US-08-313-185-58	Sequence 58, Appl
428	74.5	4.2	1148	2	US-09-082-614A-58	Sequence 58, Appl
429	74.5	4.2	1788	2	US-08-962-284-2	Sequence 2, Appl1
430	74.5	4.2	1911	1	US-08-348-006B-5	Sequence 5, Appl1
431	74.5	4.2	1911	2	US-08-800-825A-5	Sequence 5, Appl1
432	74.5	4.2	1911	3	US-09-158-657-5	Sequence 5, Appl1
433	74.5	4.2	1911	5	PCT-US94-10166-5	Sequence 84, Appl
434	74.5	4.2	4654	3	US-08-476-515A-84	Sequence 84, Appl
435	74.5	4.2	4655	3	US-08-652-877-84	Sequence 86, Appl
436	74.5	4.2	4655	3	US-08-652-877-86	Sequence 86, Appl
437	74.5	4.2	4655	3	US-08-652-877-88	Sequence 88, Appl
438	74.5	4.2	4655	3	US-08-652-877-90	Sequence 90, Appl
439	74	4.2	393	4	US-09-454-034-8	Sequence 8, Appl1
440	74	4.2	387	4	US-09-175-928-2	Sequence 2, Appl1
441	74	4.2	451	4	US-09-107-532A-6652	Sequence 6652, Ap
442	74	4.2	543	4	US-09-042-709A-18	Sequence 18, Appl
443	74	4.2	548	1	US-08-247-902A-2	Sequence 2, Appl1
444	74	4.2	548	5	PCT-US93-10541-2	Sequence 2, Appl1
445	74	4.2	862	4	US-08-556-422A-2	Sequence 2, Appl1
446	74	4.2	1027	4	US-09-162-021B-2	Sequence 2, Appl1
447	74	4.2	1333	1	US-08-447-411-76	Sequence 76, Appl
448	74	4.2	1333	2	US-08-662-227-34	Sequence 34, Appl
449	74	4.2	1333	4	US-09-017-947-34	Sequence 34, Appl
450	74	4.2	1333	4	US-09-925-442-34	Sequence 34, Appl
451	73.5	4.1	217	4	US-09-134-001C-5638	Sequence 5638, Ap
452	73.5	4.1	228	4	US-08-978-289-10	Sequence 10, Appl
453	73.5	4.1	321	4	US-09-171-461-22	Sequence 22, Appl
454	73.5	4.1	344	4	US-09-700-397-3	Sequence 3, Appl1
455	73.5	4.1	534	4	US-09-910-174B-18	Sequence 18, Appl
456	73.5	4.1	513	4	US-09-620-461-18	Sequence 18, Appl
457	73.5	4.1	699	4	US-09-620-461-18	Sequence 18, Appl
458	73.5	4.1	716	3	US-09-171-945-125	Sequence 125, App
459	73.5	4.1	913	1	US-08-445-640-4	Sequence 4, Appl1
460	73.5	4.1	913	3	US-08-170-558-4	Sequence 4, Appl1
461	73.5	4.1	913	3	US-08-447-314-4	Sequence 4, Appl1
462	73.5	4.1	913	3	US-08-445-461-4	Sequence 4, Appl1
463	73.5	4.1	1000	4	US-09-193-562D-30	Sequence 30, Appl
464	73.5	4.1	4544	1	US-08-469-486-52	Sequence 52, Appl
465	73.5	4.1	4544	2	US-08-469-658-52	Sequence 52, Appl
466	73	4.1	112	3	US-08-545-809A-136	Sequence 136, App
467	73	4.1	389	4	US-08-724-378D-7	Sequence 7, Appl1
468	73	4.1	459	1	US-08-157-101A-7	Sequence 7, Appl1
469	73	4.1	501	2	US-08-408-092-31	Sequence 31, Appl
470	73	4.1	504	4	US-08-868-373-6	Sequence 12, Appl
471	73	4.1	548	4	US-09-398-395A-12	Sequence 12, Appl
472	73	4.1	548	4	US-09-887-586A-12	Sequence 12, Appl
473	73	4.1	548	4	US-09-895-752-12	Sequence 12, Appl
474	73	4.1	548	4	US-09-903-012B-12	Sequence 12, Appl
475	73	4.1	651	3	US-08-985-950-22	Sequence 22, Appl
476	73	4.1	651	3	US-08-985-950-22	Sequence 22, Appl
477	73	4.1	293	6	US-09-546-049-22	Sequence 22, Appl
478	72.5	4.1	331	1	US-08-364-081-3	Sequence 3, Appl1
479	72.5	4.1	331	1	US-08-630-552-3	Sequence 3, Appl1
480	72.5	4.1	331	1	PCT-US95-16558-3	Sequence 3, Appl1
481	72.5	4.1	347	5	US-09-667-135-4	Sequence 4, Appl1
482	72.5	4.1	347	4	US-09-667-135-4	Sequence 4, Appl1
483	72.5	4.1	354	6	5169835-4	Patent No. 5169835
484	72.5	4.1	374	3	US-08-821-994-70	Sequence 70, Appl
485	72.5	4.1	390	2	US-08-979-794A-39	Sequence 1, Appl1
486	72.5	4.1	390	4	US-09-907-125A-39	Sequence 39, Appl
487	72.5	4.1	390	4	US-09-905-125A-39	Sequence 39, Appl
488	72.5	4.1	390	4	US-09-902-775A-39	Sequence 39, Appl
489	72.5	4.1	424	6	5169835-6	Patent No. 5169835
490	72.5	4.1	489	4	US-09-134-001C-4902	Sequence 4902, Ap
491	72.5	4.1	521	2	US-08-504-048-9	Sequence 9, Appl1
492	72.5	4.1	521	2	US-08-471-570-4	Sequence 4, Appl1
493	72.5	4.1	560	4	US-09-071-035-220	Sequence 220, App
494	72.5	4.1	605	2	US-08-752-307B-8	Sequence 8, Appl1
495	72.5	4.1	605	4	US-09-707-802-8	Sequence 8, Appl1
496	72.5	4.1	605	4	US-09-991-326-8	Sequence 8, Appl1
497	72.5	4.1	627	4	US-09-071-035-218	Sequence 218, App
498	72.5	4.1	652	1	US-08-471-570-10	Sequence 10, Appl
499	72.5	4.1	659	4	US-09-134-000C-6124	Sequence 6124, Ap
500	72.5	4.1	759	4	US-09-002-285-86	Sequence 86, Appl
501	72.5	4.1	759	4	US-09-589-477-86	Sequence 86, Appl
502	72.5	4.1	768	4	US-09-489-039A-12897	Sequence 12897, A
503	72.5	4.1	790	4	US-09-543-681A-5459	Sequence 5459, Ap
504	72.5	4.1	913	4	US-09-140-378A-2	Sequence 2, Appl1
505	72.5	4.1	919	1	US-08-336-343A-2	Sequence 2, Appl1
506	72.5	4.1	1434	2	US-08-540-406-10	Sequence 10, Appl
507	72.5	4.1	1434	3	US-08-656-055-10	Sequence 10, Appl
508	72.5	4.1	1434	3	US-08-954-668-10	Sequence 10, Appl
509	72.5	4.1	1434	4	US-08-918-658-10	Sequence 10, Appl
510	72.5	4.1	1434	4	US-09-724-631-10	Sequence 10, Appl
511	72.5	4.1	1434	4	US-08-954-701A-10	Sequence 10, Appl
512	72.5	4.1	1434	5	PCT-US95-13223-10	Sequence 10, Appl
513	72	4.1	311	4	US-09-252-991A-38792	Sequence 28792, A
514	72	4.1	328	4	US-09-489-039A-13216	Sequence 13216, A
515	72	4.1	348	2	US-09-031-485-28	Sequence 28, Appl
516	72	4.1	348	2	US-08-847-429A-28	Sequence 28, Appl
517	72	4.1	348	3	US-09-065-474-28	Sequence 28, Appl
518	72	4.1	348	4	US-09-557-034-28	Sequence 28, Appl
519	72	4.1	379	4	US-09-186-276B-46	Sequence 46, Appl
520	72	4.1	379	4	US-08-842-445-46	Sequence 46, Appl
521	72	4.1	379	4	US-09-186-188B-46	Sequence 46, Appl
522	72	4.1	456	1	US-08-435-993-6	Sequence 6, Appl1
523	72	4.1	456	5	PCT-US96-06035-6	Sequence 6, Appl1
524	72	4.1	497	4	US-08-709-731A-29	Sequence 29, Appl
525	72	4.1	517	4	US-09-723-368-4	Sequence 4, Appl1
526	72	4.1	548	4	US-09-398-395A-2	Sequence 2, Appl1
527	72	4.1	548	4	US-09-887-586A-2	Sequence 2, Appl1
528	72	4.1	548	4	US-09-895-752-2	Sequence 2, Appl1
529	72	4.1	548	4	US-09-903-012B-2	Sequence 2, Appl1
530	72	4.1	548	4	US-09-900-797-2	Sequence 2, Appl1
531	72	4.1	754	2	US-08-525-864A-2	Sequence 2, Appl1
532	72	4.1	852	4	US-09-319-588C-18	Sequence 18, Appl
533	72	4.1	1297	3	US-09-540-245A-17	Sequence 17, Appl
534	72	4.1	1456	1	US-08-803-973-2	Sequence 2, Appl1
535	72	4.1	1456	1	US-08-803-973-2	Sequence 2, Appl1
536	72	4.1	1745	2	US-09-031-485-33	Sequence 33, Appl
537	72	4.1	1745	2	US-08-847-429A-33	Sequence 33, Appl
538	72	4.1	1745	3	US-09-065-474-33	Sequence 33, Appl



539	72	4.1	1745	4	US-09-557-034-33	Sequence 33, Appl	612	71	4.0	1338	4	US-09-119-014D-6	Sequence 6, Appl1
540	71.5	4.0	206	3	US-08-821-994-77	Sequence 77, Appl	613	71	4.0	1362	2	US-08-874-678-33	Sequence 33, Appl
541	71.5	4.0	248	6	5169835-15	Patent No. 5169835	614	71	4.0	1362	3	US-08-643-839-33	Sequence 33, Appl
542	71.5	4.0	327	3	US-09-173-581-5	Sequence 5, Appl1	615	71	4.0	1362	3	US-09-348-886-33	Sequence 33, Appl
543	71.5	4.0	327	3	US-09-420-915-5	Sequence 5, Appl1	616	71	4.0	1362	3	US-08-616-844-40	Sequence 40, Appl
544	71.5	4.0	384	4	US-09-552-322-2	Sequence 2, Appl1	617	71	4.0	1481	2	US-08-599-654-40	Sequence 40, Appl
545	71.5	4.0	403	4	US-09-638-649-5	Sequence 5, Appl1	618	71	4.0	1481	3	US-08-944-868A-40	Sequence 40, Appl
546	71.5	4.0	462	4	US-09-166-350-18	Sequence 18, Appl	619	71	4.0	1481	3	US-08-944-423A-40	Sequence 40, Appl
547	71.5	4.0	523	4	US-09-910-174B-11	Sequence 11, Appl	620	71	4.0	1481	3	US-08-944-496-40	Sequence 40, Appl
548	71.5	4.0	523	4	US-09-620-461-11	Sequence 11, Appl	621	71	4.0	1481	3	US-09-621-976-3942	Sequence 3942, Ap
549	71.5	4.0	608	4	US-09-095-385-4	Sequence 4, Appl1	622	70.5	4.0	138	3	US-08-922-957-1	Sequence 1, Appl1
550	71.5	4.0	746	3	US-08-434-000A-4	Sequence 4, Appl1	623	70.5	4.0	338	3	US-08-922-957-3	Sequence 3, Appl1
551	71.5	4.0	746	3	US-09-312-157-4	Sequence 4, Appl1	624	70.5	4.0	343	4	US-09-134-000C-6363	Sequence 6363, Ap
552	71.5	4.0	919	2	US-08-788-674-4	Sequence 4, Appl1	625	70.5	4.0	466	4	US-09-134-001C-3526	Sequence 3526, Ap
553	71.5	4.0	2468	4	US-09-976-594-726	Sequence 726, App	626	70.5	4.0	467	3	US-08-821-994-83	Sequence 83, Appl
554	71	4.0	107	1	US-08-425-336-125	Sequence 125, App	627	70.5	4.0	491	4	US-09-134-001C-4727	Sequence 4727, Ap
555	71	4.0	107	1	US-08-488-113B-125	Sequence 125, App	628	70.5	4.0	502	4	US-09-489-039A-8035	Sequence 8035, Ap
556	71	4.0	107	1	US-08-477-484B-125	Sequence 125, App	629	70.5	4.0	533	1	US-07-820-011A-2	Sequence 2, Appl1
557	71	4.0	107	1	US-08-107-669D-65	Sequence 65, Appl	630	70.5	4.0	533	4	US-09-470-881-3	Sequence 3, Appl1
558	71	4.0	107	1	US-08-477-788A-87	Sequence 87, Appl	631	70.5	4.0	533	5	PCT-US93-00445-2	Sequence 2, Appl1
559	71	4.0	107	2	US-08-477-531B-65	Sequence 65, Appl	632	70.5	4.0	579	4	US-09-173-151A-2	Sequence 2, Appl1
560	71	4.0	107	2	US-08-646-360-125	Sequence 125, App	633	70.5	4.0	610	4	US-09-976-954-947	Sequence 947, App
561	71	4.0	107	2	US-08-082-842A-87	Sequence 87, Appl	634	70.5	4.0	617	3	US-09-188-930-303	Sequence 303, App
562	71	4.0	107	3	US-08-839-765-125	Sequence 125, App	635	70.5	4.0	617	4	US-09-312-283C-303	Sequence 13, Appl
563	71	4.0	107	3	US-09-136-389-125	Sequence 125, App	636	70.5	4.0	668	1	US-08-232-538-13	Sequence 13, Appl
564	71	4.0	107	4	US-09-610-838-125	Sequence 125, App	637	70.5	4.0	668	2	US-08-786-164-13	Sequence 13, Appl
565	71	4.0	107	4	US-09-711-885-125	Sequence 125, App	638	70.5	4.0	686	4	US-09-173-151A-4	Sequence 4, Appl1
566	71	4.0	233	4	US-09-198-452A-244	Sequence 244, App	639	70.5	4.0	764	4	US-09-142-956B-14	Sequence 14, Appl
567	71	4.0	236	3	US-09-049-672A-7	Sequence 7, Appl1	640	70.5	4.0	767	2	US-08-674-678-2	Sequence 2, Appl1
568	71	4.0	240	1	US-08-488-113B-147	Sequence 147, App	641	70.5	4.0	767	4	US-08-643-839-2	Sequence 2, Appl1
569	71	4.0	240	1	US-08-488-113B-148	Sequence 148, App	642	70.5	4.0	767	4	US-09-348-886-2	Sequence 2, Appl1
570	71	4.0	240	1	US-08-477-484B-147	Sequence 147, App	643	70.5	4.0	788	1	US-08-232-538-15	Sequence 15, Appl
571	71	4.0	240	1	US-08-477-484B-148	Sequence 148, App	644	70.5	4.0	788	2	US-08-786-164-15	Sequence 15, Appl
572	71	4.0	240	2	US-08-646-360-147	Sequence 147, App	645	70.5	4.0	940	4	US-09-198-452A-500	Sequence 500, App
573	71	4.0	240	2	US-08-646-360-147	Sequence 147, App	646	70.5	4.0	983	4	US-09-412-554A-2	Sequence 2, Appl1
574	71	4.0	240	3	US-08-839-765-147	Sequence 147, App	647	70.5	4.0	1088	1	US-08-484-565-6	Sequence 6, Appl1
575	71	4.0	240	3	US-08-839-765-148	Sequence 148, App	648	70.5	4.0	1088	2	US-08-484-565-6	Sequence 6, Appl1
576	71	4.0	240	3	US-09-136-389-147	Sequence 147, App	649	70.5	4.0	1088	2	US-08-480-751-6	Sequence 6, Appl1
577	71	4.0	240	3	US-09-136-389-148	Sequence 148, App	650	70.5	4.0	1088	2	US-08-943-986-6	Sequence 6, Appl1
578	71	4.0	240	4	US-09-610-838-147	Sequence 147, App	651	70.5	4.0	1088	3	US-08-553-784-6	Sequence 6, Appl1
579	71	4.0	240	4	US-09-610-838-148	Sequence 148, App	652	70.5	4.0	1088	3	US-08-484-719B-6	Sequence 6, Appl1
580	71	4.0	240	4	US-09-711-485-147	Sequence 147, App	653	70.5	4.0	1088	4	US-08-484-159-6	Sequence 6, Appl1
581	71	4.0	240	4	US-09-711-485-148	Sequence 148, App	654	70.5	4.0	1356	2	US-08-810-116-8	Sequence 8, Appl1
582	71	4.0	329	4	US-09-543-681A-7089	Sequence 7089, Ap	655	70.5	4.0	1356	2	US-07-930-548A-8	Sequence 8, Appl1
583	71	4.0	344	4	US-08-504-617-2	Sequence 2, Appl1	656	70.5	4.0	1356	3	US-09-098-707A-2	Sequence 2, Appl1
584	71	4.0	615	4	US-09-297-937C-9	Sequence 9, Appl1	657	70.5	4.0	1356	3	US-09-483-539-2	Sequence 3, Appl1
585	71	4.0	647	3	US-08-753-007A-32	Sequence 32, Appl	658	70	4.0	126	3	US-09-240-274-146	Sequence 146, App
586	71	4.0	647	3	US-09-398-496-32	Sequence 32, Appl	659	70	4.0	167	3	US-08-821-994-43	Sequence 43, Appl
587	71	4.0	661	1	US-08-232-538-12	Sequence 12, Appl	660	70	4.0	313	4	US-09-252-991A-37836	Sequence 32836, A
588	71	4.0	661	2	US-08-786-164-12	Sequence 12, Appl	661	70	4.0	320	3	US-09-036-987A-14	Sequence 14, Appl
589	71	4.0	687	1	US-08-232-538-6	Sequence 6, Appl1	662	70	4.0	320	3	US-09-370-700-14	Sequence 14, Appl
590	71	4.0	687	2	US-08-786-164-6	Sequence 6, Appl1	663	70	4.0	320	4	US-09-603-207-14	Sequence 14, Appl
591	71	4.0	687	4	US-09-427-353-2	Sequence 2, Appl1	664	70	4.0	338	1	US-08-442-043A-17	Sequence 17, Appl
592	71	4.0	731	4	US-09-107-532A-6999	Sequence 6999, Ap	665	70	4.0	338	4	US-08-441-893A-17	Sequence 17, Appl
593	71	4.0	758	2	US-08-874-678-1	Sequence 1, Appl1	666	70	4.0	347	1	US-07-940-861-43	Sequence 43, Appl
594	71	4.0	758	3	US-08-643-839-1	Sequence 1, Appl1	667	70	4.0	347	1	US-08-459-512-43	Sequence 43, Appl
595	71	4.0	758	3	US-09-051-363-24	Sequence 24, Appl	668	70	4.0	347	2	US-08-459-657-43	Sequence 43, Appl
596	71	4.0	758	4	US-09-348-886-1	Sequence 1, Appl1	669	70	4.0	347	2	US-08-460-132-43	Sequence 43, Appl
597	71	4.0	780	1	US-08-232-538-14	Sequence 14, Appl	670	70	4.0	347	2	US-08-460-132-43	Sequence 43, Appl
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599	71	4.0	821	4	US-08-451-822A-13	Sequence 13, Appl	672	70	4.0	412	4	US-09-543-681A-6782	Sequence 6782, Ap
600	71	4.0	821	4	US-08-323-430-13	Sequence 13, Appl	673	70	4.0	469	3	US-08-753-007A-8	Sequence 8, Appl1
601	71	4.0	906	4	US-09-651-656-13	Sequence 13, Appl	674	70	4.0	469	3	US-09-398-395A-8	Sequence 8, Appl1
602	71	4.0	906	4	US-09-650-855-13	Sequence 13, Appl	675	70	4.0	490	4	US-09-489-039A-9610	Sequence 9610, Ap
603	71	4.0	930	4	US-09-134-001C-5314	Sequence 5314, Ap	676	70	4.0	548	4	US-09-398-395A-6	Sequence 6, Appl1
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606	71	4.0	1018	1	US-08-408-093-6	Sequence 6, Appl1	679	70	4.0	548	4	US-09-887-586A-4	Sequence 4, Appl1
607	71	4.0	1018	1	US-08-408-420A-6	Sequence 6, Appl1	680	70	4.0	548	4	US-09-887-586A-6	Sequence 6, Appl1
608	71	4.0	1018	1	US-08-714-901-6	Sequence 6, Appl1	681	70	4.0	548	4	US-09-887-586A-8	Sequence 8, Appl1
609	71	4.0	1018	3	US-08-040-741-6	Sequence 6, Appl1	682	70	4.0	548	4	US-09-887-586A-8	Sequence 8, Appl1
610	71	4.0	1276	4	US-09-297-937C-13	Sequence 13, Appl	683	70	4.0	548	4	US-09-887-586A-10	Sequence 10, Appl
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697	70	4.0	550	3	US-08-577-483-8	Sequence 8, Appl1
698	70	4.0	550	4	US-09-435-380-8	Sequence 8, Appl1
699	70	4.0	551	3	US-09-303-064-53	Sequence 53, Appl1
700	70	4.0	551	4	US-09-086-503-53	Sequence 53, Appl1

## ALIGNMENTS

RESULT 1  
US-09-149-476-483  
Sequence 483, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
EARLIER FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
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EARLIER APPLICATION NUMBER: 60/043,670  
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EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05

EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 20.5%; Score 362.5; DB 4; Length 329;  
Best Local Similarity 31.5%; Pred. No. 1.6e-30;  
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

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66 GDSETA PVVTVTHRYNRYERIHALGPYNNLVISDLRHEADGDKADINTQADPTTKRYN 125  
122 LHYEHLSPKVTYMGLOSNKNGTCVNTLTCMEHGEDEVITYWKALGOANBSHNSILP 181  
126 LOYRRLGPKITQSLMASVNGCVTLTCSVKEKKNVTYMWSPJGE-----EGNVQ 179  
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180 IFQTPEDOLTYCTAQNVPNN-SDSISAROLCADIAMGFRTHHTGLSVLAMEFLVL 238  
236 LLLSLFVLGLFLMFLKREOEYIEKKRVDICRETPNICPSGENTEXTDTIHTRTIL 295  
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291 KEPPVTVTSVQFADKMGKASTQDSKP--PETSSEIYI 328

RESULT 2  
US-08-348-792-10  
Sequence 10, Application US/08348792  
Patent No. 5576423

GENERAL INFORMATION:  
APPLICANT: Aversa, Gregorio  
APPLICANT: Chang, Chia-Chun J.  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: de Vries, Jan E.  
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,792  
FILING DATE: 02-DEC-1994  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0436  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 343 amino acids  
TYPE: amino acid









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 Db 282 AOVQKRGF---LQKLDSPF-----ADDPCTTIYAATEPVEVSQETNSITVYASVT 331  
 QY 322 MPDT 325  
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RESULT 10  
 US-09-369-248A-3  
 ; Sequence 3, Application US/09369248A  
 ; Patent No. 6620912  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Paul  
 ; APPLICANT: Ruben, Steven M.  
 ; TITLE OF INVENTION: Dendritic Enriched Secreted Lymphocyte Activation  
 ; FILE REFERENCE: PFA48PI  
 ; CURRENT APPLICATION NUMBER: US/09/369,248A  
 ; PRIOR FILING DATE: 1999-08-05  
 ; PRIOR APPLICATION NUMBER: 60/073,962  
 ; PRIOR FILING DATE: 1998-02-06  
 ; PRIOR APPLICATION NUMBER: 60/078,572  
 ; PRIOR FILING DATE: 1998-03-19  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.1  
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 ; LENGTH: 335  
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 ; ORGANISM: Homo sapiens  
 US-09-369-248A-3

Query Match 10.3%; Score 182.5; DB 4; Length 335;  
 Best Local Similarity 22.5%; Pred. No. 4.8e-11;  
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 QY 322 MPDT 325  
 Db 332 LPES 335

RESULT 11  
 US-08-348-792-8  
 ; Sequence 8, Application US/08348792  
 ; Patent No. 5576423  
 ; GENERAL INFORMATION:

APPLICANT: Avera, Gregorio  
 APPLICANT: Chang, Chia-Chun J.  
 APPLICANT: Cocks, Benjamin G.  
 APPLICANT: de Vries, Jan B.  
 TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL  
 SURFACE ANTIGENS; PROTEINS AND ANTIBODIES  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/348,792  
 FILING DATE: 02-DEC-1994  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0436  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-496-1200  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 307 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MODE: TYPE: protein  
 US-08-348-792-8

Query Match 10.2%; Score 180; DB 1; Length 307;  
 Best Local Similarity 22.6%; Pred. No. 7.8e-11;  
 Matches 76; Conservative 67; Mismatches 120; Indels 74; Gaps 17;

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 Db 178 IYICTVSNPISNNSQTFSP-----WPGCRDPSETKPAVYAGLLGVIMILIMVILQ 231  
 QY 239 SLFVLGLFLMPLKRBROEYIE--EKRRVDICRETPNICPSGENTGYDTIPHTNRIL 295  
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RESULT 12  
 US-08-462-738-8  
 ; Sequence 8, Application US/08462738  
 ; Patent No. 5977303  
 ; GENERAL INFORMATION:  
 APPLICANT: Avera, Gregorio







Thu Aug 19 15:30:01 2004

us-10-063-551-46\_1.ral

Page 15

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OM protein - protein search, using SW model

Run on: August 18, 2004, 16:00:40 ; Search time 48 Seconds  
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2190.950 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772  
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Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 700 summaries

Database : Published Applications AA:\*

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6: /cgn2\_6/prodata/2/pubppa/PCUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/2/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/2/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/2/pubppa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/prodata/2/pubppa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/prodata/2/pubppa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/prodata/2/pubppa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/prodata/2/pubppa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/2/pubppa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/2/pubppa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/2/pubppa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/prodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/prodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	335	9 US-09-732-524-2	Sequence 2, Appl1
2	1772	100.0	335	9 US-09-989-722-253	Sequence 253, App
3	1772	100.0	335	9 US-09-989-723-253	Sequence 253, App
4	1772	100.0	335	9 US-09-989-279-253	Sequence 253, App
5	1772	100.0	335	9 US-09-989-727-253	Sequence 253, App
6	1772	100.0	335	9 US-09-989-731-253	Sequence 253, App
7	1772	100.0	335	9 US-09-989-732-253	Sequence 253, App
8	1772	100.0	335	9 US-09-745-605-4	Sequence 4, Appl1
9	1772	100.0	335	9 US-09-991-073-253	Sequence 253, App
10	1772	100.0	335	9 US-09-990-442-253	Sequence 253, App
11	1772	100.0	335	9 US-09-991-163-253	Sequence 253, App
12	1772	100.0	335	9 US-09-993-604-253	Sequence 253, App
13	1772	100.0	335	9 US-09-990-456-253	Sequence 253, App
14	1772	100.0	335	9 US-09-989-721-253	Sequence 253, App
15	1772	100.0	335	9 US-09-992-598-253	Sequence 253, App

16	1772	100.0	335	9 US-09-989-293A-253	Sequence 253, App
17	1772	100.0	335	9 US-09-989-735-253	Sequence 253, App
18	1772	100.0	335	9 US-09-990-444-253	Sequence 253, App
19	1772	100.0	335	9 US-09-991-181-253	Sequence 253, App
20	1772	100.0	335	9 US-09-989-730-253	Sequence 253, App
21	1772	100.0	335	9 US-09-990-436-253	Sequence 253, App
22	1772	100.0	335	9 US-09-993-687-253	Sequence 253, App
23	1772	100.0	335	10 US-09-989-734-253	Sequence 253, App
24	1772	100.0	335	10 US-09-997-653-253	Sequence 253, App
25	1772	100.0	335	10 US-09-993-661-253	Sequence 253, App
26	1772	100.0	335	10 US-09-997-428-253	Sequence 253, App
27	1772	100.0	335	10 US-09-997-666-253	Sequence 253, App
28	1772	100.0	335	10 US-09-990-438-253	Sequence 253, App
29	1772	100.0	335	10 US-09-990-556-253	Sequence 253, App
30	1772	100.0	335	10 US-09-990-711-253	Sequence 253, App
31	1772	100.0	335	10 US-09-989-726-253	Sequence 253, App
32	1772	100.0	335	10 US-09-998-156-253	Sequence 253, App
33	1772	100.0	335	10 US-09-990-437-253	Sequence 253, App
34	1772	100.0	335	10 US-09-991-157-253	Sequence 253, App
35	1772	100.0	335	10 US-09-997-514-253	Sequence 253, App
36	1772	100.0	335	10 US-09-997-573-253	Sequence 253, App
37	1772	100.0	335	10 US-09-991-112-253	Sequence 253, App
38	1772	100.0	335	10 US-09-990-726-253	Sequence 253, App
39	1772	100.0	335	10 US-09-997-559-253	Sequence 253, App
40	1772	100.0	335	10 US-09-997-601-253	Sequence 253, App
41	1772	100.0	335	10 US-09-990-443-253	Sequence 253, App
42	1772	100.0	335	10 US-09-991-854-253	Sequence 253, App
43	1772	100.0	335	10 US-09-997-628-253	Sequence 253, App
44	1772	100.0	335	10 US-09-997-683-253	Sequence 253, App
45	1772	100.0	335	10 US-09-989-729A-253	Sequence 253, App
46	1772	100.0	335	10 US-09-997-349-253	Sequence 253, App
47	1772	100.0	335	10 US-09-997-440-253	Sequence 253, App
48	1772	100.0	335	10 US-09-990-440-253	Sequence 253, App
49	1772	100.0	335	10 US-09-993-463-253	Sequence 253, App
50	1772	100.0	335	10 US-09-997-542-253	Sequence 253, App
51	1772	100.0	335	10 US-09-993-748-253	Sequence 253, App
52	1772	100.0	335	10 US-09-990-439-253	Sequence 253, App
53	1772	100.0	335	10 US-09-990-427-253	Sequence 253, App
54	1772	100.0	335	10 US-09-989-328-253	Sequence 253, App
55	1772	100.0	335	10 US-09-993-583-253	Sequence 253, App
56	1772	100.0	335	10 US-09-941-992-253	Sequence 253, App
57	1772	100.0	335	10 US-09-992-521-253	Sequence 253, App
58	1772	100.0	335	10 US-09-997-333-253	Sequence 253, App
59	1772	100.0	335	10 US-09-997-348-253	Sequence 253, App
60	1772	100.0	335	10 US-09-998-041-253	Sequence 253, App
61	1772	100.0	335	10 US-09-997-583-253	Sequence 253, App
62	1772	100.0	335	10 US-09-997-614-253	Sequence 253, App
63	1772	100.0	335	10 US-09-989-862-253	Sequence 253, App
64	1772	100.0	335	10 US-09-997-529-253	Sequence 253, App
65	1772	100.0	335	10 US-09-989-725-253	Sequence 253, App
66	1772	100.0	335	11 US-09-989-723-253	Sequence 253, App
67	1772	100.0	335	11 US-09-992-643-253	Sequence 253, App
68	1772	100.0	335	12 US-10-206-915-192	Sequence 192, App
69	1772	100.0	335	12 US-10-199-670-192	Sequence 192, App
70	1772	100.0	335	12 US-10-201-858-192	Sequence 192, App
71	1772	100.0	335	12 US-10-263-839-110	Sequence 110, App
72	1772	100.0	335	12 US-10-205-890-192	Sequence 192, App
73	1772	100.0	335	12 US-10-208-024-192	Sequence 192, App
74	1772	100.0	335	12 US-10-201-851-192	Sequence 192, App
75	1772	100.0	335	12 US-10-063-745-46	Sequence 46, Appl1
76	1772	100.0	335	12 US-09-989-724-253	Sequence 253, App
77	1772	100.0	335	12 US-09-989-728-253	Sequence 253, App
78	1772	100.0	335	12 US-09-990-441-253	Sequence 253, App
79	1772	100.0	335	12 US-10-063-512-46	Sequence 46, Appl1
80	1772	100.0	335	12 US-10-063-513-46	Sequence 46, Appl1
81	1772	100.0	335	12 US-10-063-515-46	Sequence 46, Appl1
82	1772	100.0	335	12 US-10-063-549-46	Sequence 46, Appl1
83	1772	100.0	335	12 US-10-063-556-46	Sequence 46, Appl1
84	1772	100.0	335	12 US-10-063-551-46	Sequence 46, Appl1
85	1772	100.0	335	12 US-10-174-581-192	Sequence 192, App
86	1772	100.0	335	12 US-10-176-483-192	Sequence 192, App
87	1772	100.0	335	12 US-10-176-749-192	Sequence 192, App
88	1772	100.0	335	12 US-10-176-914-192	Sequence 192, App



235	1772	100.0	335	14	US-10-187-601-192	Sequence 192, App	1772	100.0	335	14	US-10-188-180-192	Sequence 192, App
236	1772	100.0	335	14	US-10-187-602-192	Sequence 192, App	1772	100.0	335	14	US-10-192-015-192	Sequence 192, App
237	1772	100.0	335	14	US-10-187-603-192	Sequence 192, App	1772	100.0	335	14	US-10-194-094-192	Sequence 192, App
238	1772	100.0	335	14	US-10-187-741-192	Sequence 192, App	1772	100.0	335	14	US-10-194-425-192	Sequence 192, App
239	1772	100.0	335	14	US-10-187-743-192	Sequence 192, App	1772	100.0	335	14	US-10-194-885-192	Sequence 192, App
240	1772	100.0	335	14	US-10-187-746-192	Sequence 192, App	1772	100.0	335	14	US-10-195-885-192	Sequence 192, App
241	1772	100.0	335	14	US-10-187-747-192	Sequence 192, App	1772	100.0	335	14	US-10-195-889-192	Sequence 192, App
242	1772	100.0	335	14	US-10-187-751-192	Sequence 192, App	1772	100.0	335	14	US-10-196-748-192	Sequence 192, App
243	1772	100.0	335	14	US-10-187-753-192	Sequence 192, App	1772	100.0	335	14	US-10-196-750-192	Sequence 192, App
244	1772	100.0	335	14	US-10-187-754-192	Sequence 192, App	1772	100.0	335	14	US-10-197-659-192	Sequence 192, App
245	1772	100.0	335	14	US-10-187-757-192	Sequence 192, App	1772	100.0	335	14	US-10-197-700-192	Sequence 192, App
246	1772	100.0	335	14	US-10-187-884-192	Sequence 192, App	1772	100.0	335	14	US-10-197-705-192	Sequence 192, App
247	1772	100.0	335	14	US-10-188-767-192	Sequence 192, App	1772	100.0	335	14	US-10-197-708-192	Sequence 192, App
248	1772	100.0	335	14	US-10-188-769-192	Sequence 192, App	1772	100.0	335	14	US-10-198-764-192	Sequence 192, App
249	1772	100.0	335	14	US-10-188-770-192	Sequence 192, App	1772	100.0	335	14	US-10-198-765-192	Sequence 192, App
250	1772	100.0	335	14	US-10-188-773-192	Sequence 192, App	1772	100.0	335	14	US-10-198-768-192	Sequence 192, App
251	1772	100.0	335	14	US-10-188-781-192	Sequence 192, App	1772	100.0	335	14	US-10-198-769-192	Sequence 192, App
252	1772	100.0	335	14	US-10-194-361-192	Sequence 192, App	1772	100.0	335	14	US-10-199-405-192	Sequence 192, App
253	1772	100.0	335	14	US-10-194-423-192	Sequence 192, App	1772	100.0	335	14	US-10-199-665-192	Sequence 192, App
254	1772	100.0	335	14	US-10-195-897-192	Sequence 192, App	1772	100.0	335	14	US-10-199-666-192	Sequence 192, App
255	1772	100.0	335	14	US-10-195-897-192	Sequence 192, App	1772	100.0	335	14	US-10-199-669-192	Sequence 192, App
256	1772	100.0	335	14	US-10-195-901-192	Sequence 192, App	1772	100.0	335	14	US-10-199-671-192	Sequence 192, App
257	1772	100.0	335	14	US-10-195-902-192	Sequence 192, App	1772	100.0	335	14	US-10-199-674-192	Sequence 192, App
258	1772	100.0	335	14	US-10-196-743-192	Sequence 192, App	1772	100.0	335	14	US-10-199-675-192	Sequence 192, App
259	1772	100.0	335	14	US-10-196-760-192	Sequence 192, App	1772	100.0	335	14	US-10-199-676-192	Sequence 192, App
260	1772	100.0	335	14	US-10-173-708-192	Sequence 192, App	1772	100.0	335	14	US-10-201-770-192	Sequence 192, App
261	1772	100.0	335	14	US-10-176-479-192	Sequence 192, App	1772	100.0	335	14	US-10-201-855-192	Sequence 192, App
262	1772	100.0	335	14	US-10-176-748-192	Sequence 192, App	1772	100.0	335	14	US-10-201-856-192	Sequence 192, App
263	1772	100.0	335	14	US-10-176-916-192	Sequence 192, App	1772	100.0	335	14	US-10-202-469-192	Sequence 192, App
264	1772	100.0	335	14	US-10-179-516-192	Sequence 192, App	1772	100.0	335	14	US-10-202-470-192	Sequence 192, App
265	1772	100.0	335	14	US-10-179-519-192	Sequence 192, App	1772	100.0	335	14	US-10-202-934-192	Sequence 192, App
266	1772	100.0	335	14	US-10-179-525-192	Sequence 192, App	1772	100.0	335	14	US-10-202-936-192	Sequence 192, App
267	1772	100.0	335	14	US-10-180-540-192	Sequence 192, App	1772	100.0	335	14	US-10-202-937-192	Sequence 192, App
268	1772	100.0	335	14	US-10-180-545-192	Sequence 192, App	1772	100.0	335	14	US-10-202-938-192	Sequence 192, App
269	1772	100.0	335	14	US-10-183-006-192	Sequence 192, App	1772	100.0	335	14	US-10-202-939-192	Sequence 192, App
270	1772	100.0	335	14	US-10-183-008-192	Sequence 192, App	1772	100.0	335	14	US-10-202-940-192	Sequence 192, App
271	1772	100.0	335	14	US-10-183-017-192	Sequence 192, App	1772	100.0	335	14	US-10-202-941-192	Sequence 192, App
272	1772	100.0	335	14	US-10-183-019-192	Sequence 192, App	1772	100.0	335	14	US-10-202-942-192	Sequence 192, App
273	1772	100.0	335	14	US-10-184-618-192	Sequence 192, App	1772	100.0	335	14	US-10-202-943-192	Sequence 192, App
274	1772	100.0	335	14	US-10-184-625-192	Sequence 192, App	1772	100.0	335	14	US-10-202-944-192	Sequence 192, App
275	1772	100.0	335	14	US-10-184-625-192	Sequence 192, App	1772	100.0	335	14	US-10-202-945-192	Sequence 192, App
276	1772	100.0	335	14	US-10-184-627-192	Sequence 192, App	1772	100.0	335	14	US-10-202-946-192	Sequence 192, App
277	1772	100.0	335	14	US-10-184-645-192	Sequence 192, App	1772	100.0	335	14	US-10-202-947-192	Sequence 192, App
278	1772	100.0	335	14	US-10-184-654-192	Sequence 192, App	1772	100.0	335	14	US-10-202-948-192	Sequence 192, App
279	1772	100.0	335	14	US-10-184-655-192	Sequence 192, App	1772	100.0	335	14	US-10-202-949-192	Sequence 192, App
280	1772	100.0	335	14	US-10-188-774-192	Sequence 192, App	1772	100.0	335	14	US-10-202-950-192	Sequence 192, App
281	1772	100.0	335	14	US-10-188-775-192	Sequence 192, App	1772	100.0	335	14	US-10-202-951-192	Sequence 192, App
282	1772	100.0	335	14	US-10-184-462-192	Sequence 192, App	1772	100.0	335	14	US-10-202-952-192	Sequence 192, App
283	1772	100.0	335	14	US-10-196-745-192	Sequence 192, App	1772	100.0	335	14	US-10-202-953-192	Sequence 192, App
284	1772	100.0	335	14	US-10-196-762-192	Sequence 192, App	1772	100.0	335	14	US-10-202-954-192	Sequence 192, App
285	1772	100.0	335	14	US-10-197-695-192	Sequence 192, App	1772	100.0	335	14	US-10-202-955-192	Sequence 192, App
286	1772	100.0	335	14	US-10-197-695-192	Sequence 192, App	1772	100.0	335	14	US-10-202-956-192	Sequence 192, App
287	1772	100.0	335	14	US-10-195-894-192	Sequence 192, App	1772	100.0	335	14	US-10-202-957-192	Sequence 192, App
288	1772	100.0	335	14	US-10-176-484-192	Sequence 192, App	1772	100.0	335	14	US-10-202-958-192	Sequence 192, App
289	1772	100.0	335	14	US-10-176-484-192	Sequence 192, App	1772	100.0	335	14	US-10-202-959-192	Sequence 192, App
290	1772	100.0	335	14	US-10-176-917-192	Sequence 192, App	1772	100.0	335	14	US-10-202-960-192	Sequence 192, App
291	1772	100.0	335	14	US-10-176-982-192	Sequence 192, App	1772	100.0	335	14	US-10-202-961-192	Sequence 192, App
292	1772	100.0	335	14	US-10-179-506-192	Sequence 192, App	1772	100.0	335	14	US-10-202-962-192	Sequence 192, App
293	1772	100.0	335	14	US-10-179-513-192	Sequence 192, App	1772	100.0	335	14	US-10-202-963-192	Sequence 192, App
294	1772	100.0	335	14	US-10-179-514-192	Sequence 192, App	1772	100.0	335	14	US-10-202-964-192	Sequence 192, App
295	1772	100.0	335	14	US-10-179-522-192	Sequence 192, App	1772	100.0	335	14	US-10-202-965-192	Sequence 192, App
296	1772	100.0	335	14	US-10-180-560-192	Sequence 192, App	1772	100.0	335	14	US-10-202-966-192	Sequence 192, App
297	1772	100.0	335	14	US-10-180-560-192	Sequence 192, App	1772	100.0	335	14	US-10-202-967-192	Sequence 192, App
298	1772	100.0	335	14	US-10-183-015-192	Sequence 192, App	1772	100.0	335	14	US-10-202-968-192	Sequence 192, App
299	1772	100.0	335	14	US-10-184-620-192	Sequence 192, App	1772	100.0	335	14	US-10-202-969-192	Sequence 192, App
300	1772	100.0	335	14	US-10-184-620-192	Sequence 192, App	1772	100.0	335	14	US-10-202-970-192	Sequence 192, App
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303	1772	100.0	335	14	US-10-192-010-192	Sequence 192, App	1772	100.0	335	14	US-10-202-973-192	Sequence 192, App
304	1772	100.0	335	14	US-10-205-908-192	Sequence 192, App	1772	100.0	335	14	US-10-202-974-192	Sequence 192, App
305	1772	100.0	335	14	US-10-063-518-46	Sequence 46, App	1772	100.0	335	14	US-10-202-975-192	Sequence 192, App
306	1772	100.0	335	14	US-10-184-619-192	Sequence 192, App	1772	100.0	335	14	US-10-202-976-192	Sequence 192, App
307	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-977-192	Sequence 192, App
308	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-978-192	Sequence 192, App
309	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-979-192	Sequence 192, App
310	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-980-192	Sequence 192, App
311	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-981-192	Sequence 192, App
312	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-982-192	Sequence 192, App
313	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-983-192	Sequence 192, App
314	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-984-192	Sequence 192, App
315	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-985-192	Sequence 192, App
316	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-986-192	Sequence 192, App
317	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-987-192	Sequence 192, App
318	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-202-988-192	Sequence 192, App
319	1772	100.0	335	14	US-10-187-959-192	Sequence 192, App	1772	100.0	335	14	US-10-20	





527	1772	100.0	335	14	US-10-179-520-192	Sequence 192, App	600	1772	100.0	335	14	US-10-173-704-192	Sequence 192, App
528	1772	100.0	335	14	US-10-201-325-192	Sequence 192, App	601	1772	100.0	335	14	US-10-174-574-192	Sequence 192, App
529	1772	100.0	335	14	US-10-202-941-192	Sequence 192, App	602	1772	100.0	335	14	US-10-176-486-192	Sequence 192, App
530	1772	100.0	335	14	US-10-205-910-192	Sequence 192, App	603	1772	100.0	335	14	US-10-176-490-192	Sequence 192, App
531	1772	100.0	335	14	US-10-173-526-192	Sequence 192, App	604	1772	100.0	335	14	US-10-176-752-192	Sequence 192, App
532	1772	100.0	335	14	US-10-173-701-192	Sequence 192, App	605	1772	100.0	335	14	US-10-176-981-192	Sequence 192, App
533	1772	100.0	335	14	US-10-179-511-192	Sequence 192, App	606	1772	100.0	335	14	US-10-176-983-192	Sequence 192, App
534	1772	100.0	335	14	US-10-179-518-192	Sequence 192, App	607	1772	100.0	335	14	US-10-176-988-192	Sequence 192, App
535	1772	100.0	335	14	US-10-183-018-192	Sequence 192, App	608	1772	100.0	335	14	US-10-179-517-192	Sequence 192, App
536	1772	100.0	335	14	US-10-184-624-192	Sequence 192, App	609	1772	100.0	335	14	US-10-179-521-192	Sequence 192, App
537	1772	100.0	335	14	US-10-184-657-192	Sequence 192, App	610	1772	100.0	335	14	US-10-063-526-46	Sequence 46, App1
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540	1772	100.0	335	14	US-10-201-857-192	Sequence 192, App	613	1772	100.0	335	14	US-10-063-664-46	Sequence 46, App1
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553	1772	100.0	335	14	US-10-063-585-46	Sequence 46, App1	626	1772	100.0	335	14	US-10-063-694-46	Sequence 46, App1
554	1772	100.0	335	14	US-10-184-613-192	Sequence 192, App	627	1772	100.0	335	14	US-10-063-698-46	Sequence 46, App1
555	1772	100.0	335	14	US-10-187-739-192	Sequence 192, App	628	1772	100.0	335	14	US-10-063-699-46	Sequence 46, App1
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557	1772	100.0	335	14	US-10-183-009-192	Sequence 192, App	630	1772	100.0	335	14	US-10-063-705-46	Sequence 46, App1
558	1772	100.0	335	14	US-10-187-755-192	Sequence 192, App	631	1772	100.0	335	14	US-10-063-707-46	Sequence 46, App1
559	1772	100.0	335	14	US-10-063-588-46	Sequence 46, App1	632	1772	100.0	335	14	US-10-063-709-46	Sequence 46, App1
560	1772	100.0	335	14	US-10-063-735-46	Sequence 46, App1	633	1772	100.0	335	14	US-10-063-713-46	Sequence 46, App1
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562	1772	100.0	335	14	US-10-187-749-192	Sequence 192, App	635	1772	100.0	335	14	US-10-063-727-46	Sequence 46, App1
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568	1772	100.0	335	14	US-10-173-691-192	Sequence 192, App	641	1772	100.0	335	14	US-10-063-744-46	Sequence 46, App1
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572	1772	100.0	335	14	US-10-173-707-192	Sequence 192, App	645	1772	100.0	335	14	US-10-063-591-46	Sequence 46, App1
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574	1772	100.0	335	14	US-10-174-583-192	Sequence 192, App	647	1772	100.0	335	14	US-10-063-673-46	Sequence 46, App1
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580	1772	100.0	335	14	US-10-175-744-192	Sequence 192, App	653	1772	100.0	335	14	US-10-063-716-46	Sequence 46, App1
581	1772	100.0	335	14	US-10-175-745-192	Sequence 192, App	654	1772	100.0	335	14	US-10-063-731-46	Sequence 46, App1
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597	1772	100.0	335	14	US-10-173-692-192	Sequence 192, App	670	1772	100.0	335	14	US-10-063-604-46	Sequence 46, App1
598	1772	100.0	335	14	US-10-173-702-192	Sequence 192, App	671	1772	100.0	335	14	US-10-063-607-46	Sequence 46, App1
599	1772	100.0	335	14	US-10-173-703-192	Sequence 192, App	672	1772	100.0	335	14	US-10-063-612-46	Sequence 46, App1

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700 1772 100.0 335 15 US-10-205-506-192 Sequence 192, App

## ALIGNMENTS

RESULT 1  
US-09-732-524-2  
Sequence 2, Application US/09732524  
Patent No. US2002004193A1  
GENERAL INFORMATION:  
APPLICANT: Khodadoust, Mehran  
TITLE OF INVENTION: NOVEL MP-7 PROTEIN AND NUCLEIC ACID MOLECULES  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/732,524  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/261,759  
FILING DATE:  
APPLICATION DATA: 60/090,579  
FILING DATE: 1998-JUN-25  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-048CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 335 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-732-524-2  
Query Match  
Best Local Similarity 100.0%; Score 1772; DB 9; Length 335;  
Matched 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 241 PVLGFLPFLPKREROEYIEKKRVDICRETPNICPHSGENTGYDITPHTRTIKEDPA 300  
241 PVLGFLPFLPKREROEYIEKKRVDICRETPNICPHSGENTGYDITPHTRTIKEDPA 300  
QY 301 NTVYSTVEIPKXENPHSLTWPDPRLPAYENV 335  
301 NTVYSTVEIPKXENPHSLTWPDPRLPAYENV 335  
DB 301 NTVYSTVEIPKXENPHSLTWPDPRLPAYENV 335  
RESULT 2  
US-09-989-722-253  
Sequence 253, Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17



/ PRIOR APPLICATION NUMBER: 60/091360  
/ PRIOR FILING DATE: 1998-07-01  
/ PRIOR APPLICATION NUMBER: 60/091478  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091544  
/ PRIOR FILING DATE: 1998-07-01  
/ PRIOR APPLICATION NUMBER: 60/091519  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091626  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091633  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091978  
/ PRIOR FILING DATE: 1998-07-07  
/ PRIOR APPLICATION NUMBER: 60/091982  
/ PRIOR FILING DATE: 1998-07-07  
/ PRIOR APPLICATION NUMBER: 60/092182  
/ PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9, 8e-168;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 VLVHVEHLKRPKYTMGLQSNKNGCTVNTLTCCEHGEEDVITYTKLGAANESHNGSL 180  
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DB 181 PISMRKESDWMFTICVARNPVSRNFSPLARKLCEGAADDDPSSWVLLCLLVPLLSL 240  
QY 241 FVLGLFLMFLKREROEYIEKKRVICRETPNICHSGBENYDITPHNTTILKEDPA 300  
DB 241 FVLGLFLMFLKREROEYIEKKRVICRETPNICHSGBENYDITPHNTTILKEDPA 300  
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DB 301 NTVYSTVEIPIKGMENPHSLTWPDPTRLPAYENV 335

RESULT 3  
US-09-989-723-253  
/ Sequence 253, Application US/09989723  
/ Patent No. US20020072092A1

/ GENERAL INFORMATION:

/ APPLICANT: Ashkenazi, Avi J.  
/ APPLICANT: Baker, Kevin P.  
/ APPLICANT: Botstein, David  
/ APPLICANT: Desnoyers, Luc  
/ APPLICANT: Eaton, Dan L.  
/ APPLICANT: Ferrara, Napoleone  
/ APPLICANT: Fong, Sherman  
/ APPLICANT: Gerber, Hanspeter  
/ APPLICANT: Gerlitsen, Mary E.  
/ APPLICANT: Goddard, Audrey  
/ APPLICANT: Godowski, Paul J.  
/ APPLICANT: Grimaldi, J. Christopher  
/ APPLICANT: Gurney, Austen L.  
/ APPLICANT: Kljavin, Ivar J.  
/ APPLICANT: Napier, Mary A.  
/ APPLICANT: Pan, James  
/ APPLICANT: Paoni, Nicholas F.  
/ APPLICANT: Roy, Margaret Ann  
/ APPLICANT: Stewart, Timothy A.  
/ APPLICANT: Tumas, Daniel

/ APPLICANT: Watanabe, Colin K.  
/ APPLICANT: Williams, P. Mickey  
/ APPLICANT: Wood, William I.  
/ APPLICANT: Zhang, Zemin  
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
/ FILE REFERENCE: P2730PIC62  
/ CURRENT APPLICATION NUMBER: US/09/989,723  
/ PRIOR APPLICATION NUMBER: 60/049787  
/ PRIOR FILING DATE: 1997-06-16  
/ PRIOR APPLICATION NUMBER: 60/062250  
/ PRIOR FILING DATE: 1997-10-17  
/ PRIOR APPLICATION NUMBER: 60/065186  
/ PRIOR FILING DATE: 1997-11-12  
/ PRIOR APPLICATION NUMBER: 60/065311  
/ PRIOR FILING DATE: 1997-11-13  
/ PRIOR APPLICATION NUMBER: 60/066770  
/ PRIOR FILING DATE: 1997-11-24  
/ PRIOR APPLICATION NUMBER: 60/075945  
/ PRIOR FILING DATE: 1998-02-25  
/ PRIOR APPLICATION NUMBER: 60/078910  
/ PRIOR FILING DATE: 1998-03-20  
/ PRIOR APPLICATION NUMBER: 60/083322  
/ PRIOR FILING DATE: 1998-04-28  
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/ PRIOR APPLICATION NUMBER: 60/087827  
/ PRIOR FILING DATE: 1998-06-03  
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/ PRIOR FILING DATE: 1998-06-04  
/ PRIOR APPLICATION NUMBER: 60/088025  
/ PRIOR FILING DATE: 1998-06-04  
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/ PRIOR FILING DATE: 1998-06-05  
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/ PRIOR FILING DATE: 1998-06-09  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9, 8e-168;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSPCTLTLYIYLMQTSAAAGPYKELVGSVGAVTPLSKVQVDSIVMTFNTPL 60  
DB 1 MASSPTCLTYIYLMQTSAAAGPYKELVGSVGAVTPLSKVQVDSIVMTFNTPL 60  
QY 61 VTIQPEGGTTIYVONNRERVDPPDGYSLKSLKXNDGIIYVGIYSSLSQPSIOEX 120  
DB 61 VTIQPEGGTTIYVONNRERVDPPDGYSLKSLKXNDGIIYVGIYSSLSQPSIOEX 120  
QY 121 VLVHYEHLKSKPYTGMGLQSNKGTCTNLTCCMEHEBEDVIYWKALGQANSHNGSIL 180  
DB 121 VLVHYEHLKSKPYTGMGLQSNKGTCTNLTCCMEHEBEDVIYWKALGQANSHNGSIL 180  
QY 181 PISMRGESDMFTICVARNPVSNFSSPILARLCEGAADDPSSWVLLCLLVPLLSL 240  
DB 181 PISMRGESDMFTICVARNPVSNFSSPILARLCEGAADDPSSWVLLCLLVPLLSL 240  
QY 241 FVLGLFLWFLKREOREYIEEKRVDICRETPNICPHSGENTBYDTIPHTNRTILKEDPA 300  
DB 241 FVLGLFLWFLKREOREYIEEKRVDICRETPNICPHSGENTBYDTIPHTNRTILKEDPA 300  
QY 301 NTVYSTVEIIPKCMENPHSLTMPDTPRLPAYENV 335  
DB 301 NTVYSTVEIIPKCMENPHSLTMPDTPRLPAYENV 335

RESULT 4  
US-09-989-279-253  
Sequence 253, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C56  
CURRENT APPLICATION NUMBER: US/09/989,279  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9, 8e-168;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VTIQPEGGIIYVQNRREKRVDPDGGYSLKSLKKNDSGIYVVGIVSSLSLOOPISTQEX 120  
DB 61 VTIQPEGGIIYVQNRREKRVDPDGGYSLKSLKKNDSGIYVVGIVSSLSLOOPISTQEX 120  
QY 121 VLVHYEHLSPKVTMGLQSNKNGTCVTNLTCCMEHGEDEVITYWKALQGANESHNGSIL 180  
DB 121 VLVHYEHLSPKVTMGLQSNKNGTCVTNLTCCMEHGEDEVITYWKALQGANESHNGSIL 180  
QY 181 PISWRMESDMTFCVARNVSRNFSPIIARLCEGAADDPSSMWLCLLVLPLLSL 240  
DB 181 PISWRMESDMTFCVARNVSRNFSPIIARLCEGAADDPSSMWLCLLVLPLLSL 240  
QY 241 FVLGLFMPFKREGEYIEEKQKVDICRETPTNICPSGENTEXDTIPTNRTILKEDPA 300  
DB 241 FVLGLFMPFKREGEYIEEKQKVDICRETPTNICPSGENTEXDTIPTNRTILKEDPA 300  
QY 301 NTYVSTVEIPKKNENPHSLLTMPDTPPLFAVENVI 335  
DB 301 NTYVSTVEIPKKNENPHSLLTMPDTPPLFAVENVI 335

RESULT 5  
US-09-989-727-253  
Sequence 253, Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Gurney, Austin L.  
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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1065  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091787
PRIOR FILING DATE: 1998-07-07	PRIOR APPLICATION NUMBER: 60/091962
PRIOR FILING DATE: 1998-07-07	PRIOR APPLICATION NUMBER: 60/092162
PRIOR FILING DATE: 1998-07-09	PRIOR APPLICATION NUMBER: 60/092162

Query Match	100.0%;	Score 1772;	DB 9;	Length 335;
Best Local Similarity	100.0%;	Pred. No. 9.8e-168;		
Matches 335;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MAGSPCLLTLLIYLLMQLTGSAAASGPVELVOSVCGAATPPLKSKVKQVDSIWTFTPTPL	60
Db	1	MAGSPCLLTLLIYLLMQLTGSAAASGPVELVOSVCGAATPPLKSKVKQVDSIWTFTPTPL	60
QY	61	YLTQREGGTIIYLTQNRNRERVPDGGISLKLSTLKNDSGIYYVGYSSLTQOSTOEY	120
Db	61	YLTQREGGTIIYLTQNRNRERVPDGGISLKLSTLKNDSGIYYVGYSSLTQOSTOEY	120
QY	121	VLYVYEHLSKPKVTYMGLOSNNQGTCTVNTLTCCMHGSEDIYITMKALGQANNSHNGSLI	180
Db	121	VLYVYEHLSKPKVTYMGLOSNNQGTCTVNTLTCCMHGSEDIYITMKALGQANNSHNGSLI	180



QY 181 PISRWGESDPTFCVARNPVSRNPSRPILARKLCRGAADDPSSMWLLCLLVPILSL 240  
DB 181 PISRWGESDPTFCVARNPVSRNPSRPILARKLCRGAADDPSSMWLLCLLVPILSL 240  
QY 241 FVLGLFLMPLKREKREBEYIESEKKRVDICRETPNICPSGENTEXTDTPHTNRITLKEDPA 300  
DB 241 FVLGLFLMPLKREKREBEYIESEKKRVDICRETPNICPSGENTEXTDTPHTNRITLKEDPA 300  
QY 301 NTYVSTVEIRPKKMPHSLTLMPTPLFAVENVI 335  
DB 301 NTYVSTVEIRPKKMPHSLTLMPTPLFAVENVI 335  
RESULT 6  
US-09-989-731-253  
Sequence 253, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavits, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989, 731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
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PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089522  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18

;; PRIOR APPLICATION NUMBER: 60/089947  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089948  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089952  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090246  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090252  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090254  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090355  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090535  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090540  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090542  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090676  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090695  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090862  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9,8e-168;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAGSPCTLLIYILMQLGSAASGPKVKEIVSGVAVTPPLSKSKYKOYDSITWTFNTPL 60  
DB 1 MAGSPCTLLIYILMQLGSAASGPKVKEIVSGVAVTPPLSKSKYKOYDSITWTFNTPL 60  
QY 61 VTIOEGGIIIVTONRNERVDPPDGYSLKLSKLKNDGIIYVGIYSSIQDPSIOEY 120  
DB 61 VTIOEGGIIIVTONRNERVDPPDGYSLKLSKLKNDGIIYVGIYSSIQDPSIOEY 120  
QY 121 VLAHYEHLSPKPYTMGLSNKNGTCVTNLTCMEHGEEDVIYTMKALQOANESHNGSL 180  
DB 121 VLAHYEHLSPKPYTMGLSNKNGTCVTNLTCMEHGEEDVIYTMKALQOANESHNGSL 180  
QY 181 PISMRWGESDMTFICVANPVRNPSPIIARKLCEGAADPDSSMVLICLLVPLLSL 240  
DB 181 PISMRWGESDMTFICVANPVRNPSPIIARKLCEGAADPDSSMVLICLLVPLLSL 240  
QY 241 FVLGLFLWFLKEROEYIEKKRVDICRETPNICPHSGENTYDITIPTNRTILKEDPA 300  
DB 241 FVLGLFLWFLKEROEYIEKKRVDICRETPNICPHSGENTYDITIPTNRTILKEDPA 300  
QY 301 NTVYSTVEIPKMEHPHSLTMPDTPRLPAYENV 335  
DB 301 NTVYSTVEIPKMEHPHSLTMPDTPRLPAYENV 335

RESULT 7  
US-09-985-732-253  
; Sequence 253, Application US/09989732  
; Patent No. US20020123463A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PLC57  
; CURRENT APPLICATION NUMBER: US/09/989,732  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25



;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9, 8e-168;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLLIYILMQLTGSAAAGPVKELVSGAVTPEPLKSKVQVDSIYWTFTTPL 60  
DB 1 MAGSPTCLTLLIYILMQLTGSAAAGPVKELVSGAVTPEPLKSKVQVDSIYWTFTTPL 60  
QY 61 VTIOPEGTTIYTONNRRERVDPPDGGYSLKSLKKNDSGIYYVGIYSSSLQOPESTORY 120  
DB 61 VTIOPEGTTIYTONNRRERVDPPDGGYSLKSLKKNDSGIYYVGIYSSSLQOPESTORY 120  
QY 121 VLAHVEHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180  
DB 121 VLAHVEHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180  
QY 181 PISMRWGESDMTFCVARNPVSRNFSPIIARLCEGAADDDSSMWLLCLLVPLLSL 240  
DB 181 PISMRWGESDMTFCVARNPVSRNFSPIIARLCEGAADDDSSMWLLCLLVPLLSL 240  
QY 241 FVLGLFLWFLKREOREEYIEKKRVDICRETPNICPHSGENTEYDTIPTHNTIILKEDPA 300  
DB 241 FVLGLFLWFLKREOREEYIEKKRVDICRETPNICPHSGENTEYDTIPTHNTIILKEDPA 300  
QY 301 NTVYSTVEIIPKKMENPHSLTTPDTPRLPAYENVI 335  
DB 301 NTVYSTVEIIPKKMENPHSLTTPDTPRLPAYENVI 335

RESULT 8  
US-09-745-605-4  
; Sequence 4, Application US/09745605  
; Patent No. US20020123617A1  
; GENERAL INFORMATION:  
; APPLICANT: Stealing, Gary C.  
; APPLICANT: Finger, Joshua N.  
; TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2,  
; FILE REFERENCE: DB1JNP  
; CURRENT APPLICATION NUMBER: US/09/745,605  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/172,025  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-745-605-4

Query Match 100.0%; Score 1772; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9, 8e-168;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLLIYILMQLTGSAAAGPVKELVSGAVTPEPLKSKVQVDSIYWTFTTPL 60  
DB 1 MAGSPTCLTLLIYILMQLTGSAAAGPVKELVSGAVTPEPLKSKVQVDSIYWTFTTPL 60  
QY 61 VTIOPEGTTIYTONNRRERVDPPDGGYSLKSLKKNDSGIYYVGIYSSSLQOPESTORY 120  
DB 61 VTIOPEGTTIYTONNRRERVDPPDGGYSLKSLKKNDSGIYYVGIYSSSLQOPESTORY 120

QY 121 VLAHVEHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180  
DB 121 VLAHVEHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180  
QY 181 PISMRWGESDMTFCVARNPVSRNFSPIIARLCEGAADDDSSMWLLCLLVPLLSL 240  
DB 181 PISMRWGESDMTFCVARNPVSRNFSPIIARLCEGAADDDSSMWLLCLLVPLLSL 240  
QY 241 FVLGLFLWFLKREOREEYIEKKRVDICRETPNICPHSGENTEYDTIPTHNTIILKEDPA 300  
DB 241 FVLGLFLWFLKREOREEYIEKKRVDICRETPNICPHSGENTEYDTIPTHNTIILKEDPA 300  
QY 301 NTVYSTVEIIPKKMENPHSLTTPDTPRLPAYENVI 335  
DB 301 NTVYSTVEIIPKKMENPHSLTTPDTPRLPAYENVI 335

RESULT 9  
US-09-991-073-253  
; Sequence 253, Application US/09991073  
; Patent No. US20020127576A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Guiney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C15  
; CURRENT APPLICATION NUMBER: US/09/991,073  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607

[illegible]

; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 9, 8e-168;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTLLIYLIMOLTSASGPVKEIVGSGAVTPEPLSKVKQVDSIWTENTPL 60  
DB 1 MAGSPCTLLIYLIMOLTSASGPVKEIVGSGAVTPEPLSKVKQVDSIWTENTPL 60

QY 61 VTIQPEGGTIIYTONNRRRVPDPDGGYSLKLSKLNKNSGIIYVGIYSSSLQGPSTQRY 120  
DB 61 VTIQPEGGTIIYTONNRRRVPDPDGGYSLKLSKLNKNSGIIYVGIYSSSLQGPSTQRY 120

QY 121 VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHEGEBVIYTWKALGOAANESHNGSL 180  
DB 121 VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHEGEBVIYTWKALGOAANESHNGSL 180

QY 181 PISMRWGESDWMFTICVARNPVSRNFSPIIARKLCEGAADDPSSMWLLCLLIVPLLSL 240  
DB 181 PISMRWGESDWMFTICVARNPVSRNFSPIIARKLCEGAADDPSSMWLLCLLIVPLLSL 240

QY 241 FVLGLFLMFLKGRQREYIEBKRVVICRETPVICPSEGNTEYDTIIPHTNRTILKEDPA 300  
DB 241 FVLGLFLMFLKGRQREYIEBKRVVICRETPVICPSEGNTEYDTIIPHTNRTILKEDPA 300

QY 301 NTVYSTVEIPKKNENPHSLITMPDTPRLPAYENVI 335  
DB 301 NTVYSTVEIPKKNENPHSLITMPDTPRLPAYENVI 335

RESULT 10  
US-09-990-442-253  
; Sequence 253, Application US/09990442  
; Patent No. US2002013252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Guiney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C8  
; CURRENT APPLICATION NUMBER: US/09/990,442  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
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Qy 241 FVLGLFLMFLKREOREYEIEBKRVDICRETPNICPHSGENTERYDITPHNRTILKEDPA 300  
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Qy 301 NTYVSTVEIPKKNENPHSLTJMPDTPRLPAYENVY 335  
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RESULT 11  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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PRIOR FILING DATE: 1998-07-09

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APPLICANT: Desnoyers, Luc  
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FILE OR INVENTION: Acids Encoding the Same  
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? PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 1772; DB 9; Length 335;
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Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      301 NTVYSTVEIPKKMENPHSLTMTPTPRLFAVENVI 335
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RESULT 13
US-09-990-156-253
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Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C22  
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PROR APPLICATION NUMBER: 60/092182  
PROR FILING DATE: 1998-07-09

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QY 181 PISWMBESDMFTICVARNPVSRRNSSPLIARKLCEGAADDDSSMTLLCLLVPLLSL 240  
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## RESULT 1:

US-09-989-721-253  
Sequence 253, Application US/09989721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC55  
CURRENT APPLICATION NUMBER: US/09/989,721  
CURRENT FILING DATE: 2001-11-19  
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Qy      121  VLAHYEHLSPKPYTWGLQGNKNGTCVTNLTCCMEHGEEDVIYTWALGQANESHNGSIL 180
        121  VLAHYEHLSPKPYTWGLQGNKNGTCVTNLTCCMEHGEEDVIYTWALGQANESHNGSIL 180
Db      181  PLSMWGSDMTFCVARRPVSRNPSPIIARLCEGADDDPSSWVLLCLLVPLLLSL 240
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Qy      241  FVLGLFLWFLKREPOEYIEKKRVYDICTETPNI CPHSGENTEYDTIPTNRTIILKEDPA 300
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Db      301  NTVYSTVEIPKKNENPHSLITMPDTPRLPAYENVI 335
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RESULT 15
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; Sequence 253, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Aebkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 9, 8e-168;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 50 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: August 18, 2004, 16:05:21 ; Search time 16 Seconds  
(without alignments)  
2014.010 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772

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Scoring table: BLOSUM62

Gapop 10.0 , Gapeact 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 700 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	343	19.4	629	2 A46500	ly-9.2 antigen - m
2	182.5	10.3	335	2 S58892	signaling lymphocy
3	144	8.1	344	2 B28967	T-cell surface gly
4	138	7.8	344	2 I49585	CD2 antigen protei
5	136.5	7.7	351	1 RMHUC2	T-cell surface gly
6	134	7.6	240	2 S01299	OX-45 membrane gly
7	130	7.3	344	1 RMRTC2	T-cell surface gly
8	126.5	7.1	240	2 JL0143	antigen BCM1 precu
9	125.5	7.1	321	2 JH0395	biliary glycoprote
10	125.5	7.1	351	2 JH0396	biliary glycoprote
11	125.5	7.1	417	2 JH0394	biliary glycoprote
12	125.5	7.1	464	2 C30127	biliary glycoprote
13	125.5	7.1	526	1 A32164	transmembrane carc
14	124.5	7.0	344	2 A24781	nonspecific cross-
15	122.5	6.9	521	2 S34338	biliary glycoprote
16	119	6.7	458	2 JCI1509	biliary glycoprote
17	114.5	6.5	702	2 A36319	carcinoembryonic a
18	113.5	6.4	458	1 MMSMR1	biliary glycoprote
19	113.5	6.4	521	2 JCI1508	biliary glycoprote
20	109.5	6.2	432	2 S30193	T-cell surface gly
21	108.5	6.1	358	2 JCI7780	coxsackie- and ade
22	107.5	6.1	398	2 I49443	gene 2B4 protease -
23	106	6.0	897	2 G84633	hypothetical prote
24	105.5	6.0	329	1 A48754	B7-2 antigen - hum
25	104	5.9	349	2 A34815	carcinoembryonic a
26	102.5	5.8	458	2 S23969	cell-adhesion mole
27	102.5	5.8	526	2 A37821	butyrophilin - bov
28	101.5	5.7	761	2 T00940	hypothetical prote
29	101	5.7	587	2 JH0464	DM-GRASP precursor

30	101	5.7	588	2 JH0506	adhesion molecule
31	100.5	5.7	259	2 A86822	hypothetical prote
32	100	5.6	392	2 B44194	poliovirus recepto
33	99	5.6	417	2 A44194	poliovirus recepto
34	99	5.6	588	2 A45254	surface glycoprote
35	98.5	5.6	1227	2 T23004	hypothetical prote
36	98	5.5	347	2 S41638	T-cell surface gly
37	98	5.5	503	2 JCS287	SHP substrate-1 pr
38	97	5.5	523	2 I50478	neuroilin - goldfie
39	97	5.5	773	1 QRFBG	secretory componen
40	96.5	5.4	402	2 A40678	T-cell adhesion re
41	96	5.4	526	2 S36297	T-cell receptor ga
42	96	5.4	210	2 S70587	butyrophilin precu
43	96	5.4	1087	2 I51552	platelet-derived g
44	96	5.4	1451	2 S42167	190K protein - hum
45	95.5	5.4	341	2 UC1512	biliary glycoprote
46	95.5	5.4	417	1 RMHUPA	poliovirus recepto
47	95.5	5.4	458	2 S68177	C-CM2a protein is
48	95.5	5.4	519	2 A44783	ecto-ATPase precu
49	95.5	5.4	700	1 S12053	protein-tyrosine-p
50	94.5	5.3	218	2 A36198	T-cell receptor be
51	94	5.3	233	2 JH0372	42K surface glycop
52	94	5.3	1088	1 IJXLNL	neural cell adhesi
53	93.5	5.3	2409	1 A60979	versican precursor
54	93	5.2	419	2 A36109	pregnancy-specific
55	93	5.2	419	2 B54312	pregnancy-specific
56	93	5.2	419	2 JCA123	pregnancy-specific
57	92.5	5.2	299	2 S56749	functional adhesio
58	92.5	5.2	330	2 I46691	CD86 precursor - r
59	92.5	5.2	761	2 A96810	probable Mutator-1
60	92	5.2	822	2 T01095	hypothetical prote
61	91.5	5.2	1079	2 T28197	probable DNA-direc
62	91	5.1	417	2 A28277	pregnancy-specific
63	91	5.1	417	2 A33258	pregnancy-specific
64	91	5.1	426	2 B33258	pregnancy-specific
65	91	5.1	457	1 HLMSP3	poliovirus recepto
66	90	5.1	260	2 A28564	lymphocyte functio
67	90	5.1	395	2 D43354	pregnancy-specific
68	90	5.1	397	2 C43354	pregnancy-specific
69	90	5.1	406	2 E43354	pregnancy-specific
70	90	5.1	426	2 A31135	pregnancy-specific
71	90	5.1	419	2 A35964	pregnancy-specific
72	90	5.1	426	2 A35341	pregnancy-specific
73	90	5.1	428	2 A27658	pregnancy-specific
74	89.5	5.1	243	2 A53244	leukocyte antigen
75	89.5	5.1	349	2 E84968	outer membrane pro
76	89.5	5.1	428	2 T36565	probable penicilli
77	89	5.0	309	2 I49522	gene B7-2 protein
78	89	5.0	341	2 JCI1511	biliary glycoprote
79	89	5.0	821	1 C1HUM3	calpain (EC 3.4.22
80	89	5.0	5175	2 T20992	hypothetical prote
81	89	5.0	5198	2 T43290	hemiscentin precu
82	88.5	5.0	1390	1 TVHUME	hepatocyte growth
83	88	5.0	363	2 F70195	UDP-N-acetylglucos
84	88	5.0	432	2 A71147	hypothetical prote
85	88	5.0	530	2 A53437	poliovirus recepto
86	88	5.0	668	2 S56909	polymyxin B resist
87	88	5.0	699	2 JCI132	protein-tyrosine-p
88	88	5.0	821	1 B34488	calpain (EC 3.4.22
89	88	5.0	1092	1 JN0635	neural cell adhesi
90	88	5.0	6669	2 S55024	nebulin, skeleto
91	87.5	4.9	265	2 A55811	carcinoembryonic a
92	87.5	4.9	276	2 S20690	31.6K hypothetica
93	87.5	4.9	392	1 RMHUPD	poliovirus recepto
94	87.5	4.9	769	1 QRRTGS	secretory componen
95	87.5	4.9	2340	2 I48310	kinase-related pro
96	87.5	4.9	4162	2 T42633	connectin/citfin -
97	87	4.9	457	1 RWMST4	T-cell surface gly
98	87	4.9	583	2 I39428	alcam - human
99	87	4.9	1666	2 A48594	skeletin - mouse
100	87	4.9	1907	2 S50893	protein-tyrosine-p
101	87	4.9	3707	2 S18252	heparan sulfate pr
102	86.5	4.9	528	2 B75364	extracellular solu

103	86	4.9	212	2	C3258	pregnancy-specific glycoprotein D pre	176	80	4.5	1040	2	A49356	transient axonal g
104	86	4.9	354	1	VG867	glycoprotein-specific	177	80	4.5	1170	2	A40558	chromospondin 1 p
105	86	4.9	428	2	I57486	pregnancy-specific NBS/LRR disease re	178	79.5	4.5	134	2	I46627	rearranged T-cell
106	86	4.9	885	2	B86257	immunoglobulin-11k	179	79.5	4.5	249	1	A61087	myelin P0 glycopro
107	86	4.9	1327	2	T09402	pregnancy-specific	180	79.5	4.5	273	2	B28928	pregnancy-specific
108	85.5	4.8	324	2	G43354	pregnancy-specific	181	79.5	4.5	275	2	A28928	pregnancy-specific
109	85.5	4.8	326	2	F43354	pregnancy-specific	182	79.5	4.5	282	2	C28928	pregnancy-specific
110	85.5	4.8	333	2	A43354	pregnancy-specific	183	79.5	4.5	289	2	G90314	oxidoreductase [m
111	85.5	4.8	335	2	H43354	pregnancy-specific	184	79.5	4.5	328	2	J01121	cysteine proteins
112	85.5	4.8	941	1	TVMYMD	protein-tyrosine k	185	79.5	4.5	400	2	A10104	probable galactosi
113	85.5	4.8	2588	2	T14342	NSD1 protein - mou	186	79.5	4.5	430	2	T28143	capasin 1 homolog,
114	85	4.8	428	2	US0032	pregnancy-specific	187	79.5	4.5	446	2	T34782	probable signal pe
115	85	4.8	731	2	T16524	hypothetical prote	188	79.5	4.5	490	2	I41293	EcoE type I restri
116	85	4.8	757	1	S48841	secretory componen	189	79.5	4.5	769	2	S16236	fibroblast growth
117	84.5	4.8	656	2	A96724	hypothetical prote	190	79.5	4.5	822	2	A45081	keratinocyte growt
118	84	4.7	275	2	JC7604	CD86 spliced varia	191	79.5	4.5	822	2	A41794	VLU receptor prec
119	84	4.7	851	2	D90216	hypothetical prote	192	79.5	4.5	873	1	I48952	macrophage colony-
120	84	4.7	1379	1	S01254	hepatocyte growth	193	79.5	4.5	980	1	TVCTMD	165k protein, skel
121	84	4.7	1499	2	I50212	protein-tyrosine-p	194	79.5	4.5	1465	2	S43529	insulin-like growt
122	84	4.7	3034	2	T14119	seven-pass transme	195	79.5	4.5	2491	1	A28372	hypothetical prote
123	83.5	4.7	315	2	H71009	probable prolifera	196	79.5	4.5	210	2	C87256	hypothetical prote
124	83.5	4.7	392	2	T33444	hypothetical prote	197	79	4.5	244	2	AC1765	B. subtilis Taga p
125	83.5	4.7	656	2	B49423	semaphorin I - fru	198	79	4.5	438	2	G64513	hypothetical prote
126	83.5	4.7	775	2	T21436	hypothetical prote	199	79	4.5	479	2	G84099	carboxy-terminal p
127	83.5	4.7	1501	2	I58148	protein-tyrosine-p	200	79	4.5	584	2	T08678	hypothetical prote
128	83.5	4.7	1863	2	S46217	protein-tyrosine-p	201	79	4.5	657	2	S77543	short-chain alcoho
129	83	4.7	335	2	A33514	pregnancy-specific	202	79	4.5	903	2	T20804	hypothetical prote
130	83	4.7	757	2	I45956	polymetric immunog	203	79	4.5	1228	2	G96751	hypothetical prote
131	83	4.7	873	1	A49729	VLDL receptor prec	204	79	4.5	1361	2	T30884	neural specific DN
132	83	4.7	925	2	T37475	lipoprotein recept	205	78.5	4.4	235	2	S25750	Ig lambda chain -
133	83	4.7	1106	2	T29496	hypothetical prote	206	78.5	4.4	429	1	EHRT	Ig epsilon chain C
134	83	4.7	2489	2	S59782	probable membrane	207	78.5	4.4	497	2	C91225	probable oxidoredu
135	82.5	4.7	393	2	B96780	hypothetical prote	208	78.5	4.4	539	2	T01513	CTP synthase (EC 6
136	82.5	4.7	826	2	B36203	iron-responsive el	209	78.5	4.4	588	2	I37202	B-CAM protein - hu
137	82.5	4.7	1004	2	A71617	SERA antigen/papai	210	78.5	4.4	628	2	I38000	Lutheran blood gro
138	82.5	4.7	26926	1	I38344	lctin, cardiac mus	211	78.5	4.4	638	2	T51383	receptor protein k
139	82	4.6	386	2	B69666	hemagglutinin - ri	212	78.5	4.4	831	2	S39835	hypothetical prote
140	82	4.6	609	2	S43009	protein-tyrosine k	213	78.5	4.4	847	2	JH0371	B-cell adhesion pr
141	82	4.6	880	2	B53743	chondroitin sulfat	214	78.5	4.4	1036	2	S22383	axotin 1 precursor
142	82	4.6	3562	2	A47171	OX-2 membrane gly	215	78.5	4.4	1038	2	A62187	hypothetical prote
143	81.5	4.6	378	1	TDRXOX	pregnancy-specific	216	78.5	4.4	1468	2	T05672	undecaprenyl pyro
144	81.5	4.6	352	2	I77374	cysteine proteins	217	78.5	4.4	257	2	A97121	biliary glycoprote
145	81.5	4.6	355	2	T06122	leukostallin precu	218	78	4.4	272	2	I48268	carcinoembryonic a
146	81.5	4.6	378	2	S00842	galactose-1-phosph	219	78	4.4	286	2	A28332	pregnancy-specific
147	81.5	4.6	497	2	D97264	flagellin - Shigel	220	78	4.4	335	2	CS4312	probable advanced
148	81.5	4.6	524	2	S44982	hypothetical prote	221	78	4.4	402	2	T09062	DEAD box ATP-depen
149	81.5	4.6	708	2	T48022	nonspecific cross-	222	78	4.4	490	2	T43184	gTP-binding protei
150	81	4.6	335	2	B33251	limbic-system-asso	223	78	4.4	604	2	T41249	hemagglutinin - ri
151	81	4.6	338	2	JC4776	naringenin 3-dioxy	224	78	4.4	608	2	AB3562	neural cell adhesi
152	81	4.6	374	2	S57750	probable membrane	225	78	4.4	609	1	HNNZKA	hypothetical prote
153	81	4.6	760	2	S19374	glycosyltransferas	226	78	4.4	761	1	IYHUNG	cadherin 3 precurs
154	81	4.6	769	2	E97092	leukocyte antigen-	227	78	4.4	836	2	T42323	probable vacuolar
155	81	4.6	829	1	IYHUCP	ubiquitin-protein	228	78	4.4	905	2	S43064	hypothetical prote
156	81	4.6	1898	2	S46216	elk ligand - human	229	78	4.4	905	2	T34324	conserved hypotet
157	81	4.6	1941	2	T30554	UDP-N-acetylmuram	230	78	4.4	172	2	T34227	CDB alpha chain -
158	80.5	4.5	346	2	S46993	pregnancy-specific	231	77.5	4.4	448	2	H98007	exodeoxyribonuclea
159	80.5	4.5	376	2	E85435	probable transpor	232	77.5	4.4	509	2	JC5288	SNP substrate-1 pr
160	80.5	4.5	462	2	H97292	membrane protei	233	77.5	4.4	513	2	G86465	glucanate dehydrog
161	80.5	4.5	473	2	AG0612	probable acylamino	234	77.5	4.4	236	2	T41012	ferrienterobactin-
162	80.5	4.5	475	2	I76668	plus fringe glycop	235	77.5	4.4	239	2	T46082	neuraxin - rat
163	80.5	4.5	540	2	H90751	ZK112.7 protein -	236	77.5	4.4	717	2	AB3097	hypothetical prote
164	80.5	4.5	540	2	F85615	protein UNC-89 - C	237	77.5	4.4	739	2	A41288	vascular cell adhe
165	80.5	4.5	540	2	B64829	T-cell receptor be	238	77.5	4.4	863	2	S64742	dynamin-related pr
166	80.5	4.5	540	2	B64829	membrane protei	239	77.5	4.4	863	2	S64742	neuraxin - rat
167	80.5	4.5	721	2	T09631	probable acylamino	240	77.5	4.4	881	2	S03068	hypothetical prote
168	80.5	4.5	823	2	T08092	periplasmic ferric	241	77.5	4.4	968	2	T25667	polynucleotide pho
169	80.5	4.5	823	2	S44887	Ig mu chain C regi	242	77.5	4.4	991	2	T48631	hypothetical prote
170	80	4.5	307	1	T29577	arginine/ornithine	243	77.5	4.4	1015	2	T32186	
171	80	4.5	341	2	I61725		244	77.5	4.4				
172	80	4.5	343	2	G90680		245	77.5	4.4				
173	80	4.5	343	2	C85531		246	77.5	4.4				
174	80	4.5	454	2	A46532		247	77.5	4.4				
175	80	4.5	482	2	JH0110		248	77.5	4.4				

249	77.5	4.4	1099	2	T18713	hypotheical prote	322	76	4.3	1018	2	UC4211	neural adhesion pr
250	77.5	4.4	1205	2	T13959	timelese protein T	323	76	4.3	1093	2	T51503	valine-tRNA ligase
251	77.5	4.4	1262	1	B48758	protein-tyrosine-p	324	76	4.3	2029	1	TDFPLK	protein-tyrosine-p
252	77.5	4.4	1496	1	A48758	protein-tyrosine-p	325	75.5	4.3	246	2	A47712	myelin/oligodendro
253	77.5	4.4	1894	2	C54689	protein-tyrosine-p	326	75.5	4.3	326	2	UC4124	pregnancy-specific
254	77.5	4.4	1912	2	A56178	protein-tyrosine-p	327	75.5	4.3	419	2	S42989	T48 protein - fru1
255	77.5	4.4	1950	2	S12332	ubiquitin-protein	328	75.5	4.3	421	2	T40614	G beta repeat prot
256	77	4.3	1950	2	S06611	Ig gamma-2 chain C	329	75.5	4.3	432	2	T31030	hypotheical prote
257	77	4.3	328	2	I47158	Ig gamma 1 chain C	330	75.5	4.3	446	2	A95140	exodeoxyribonuclea
258	77	4.3	338	2	UC5519	50K glycoprotein p	331	75.5	4.3	462	2	A84689	chloroplast membra
259	77	4.3	338	2	B86353	protein F282.6 [im	332	75.5	4.3	485	2	T28076	hypotheical prote
260	77	4.3	439	2	S51378	volage-gated pote	333	75.5	4.3	819	2	T05744	hypotheical prote
261	77	4.3	491	2	JE0276	SKS1 protein - yea	334	75.5	4.3	933	2	H69045	neuronai cell surf
262	77	4.3	502	2	S61935	cytochrome P450 78	335	75.5	4.3	1020	1	S05944	aggreacan precuroe
263	77	4.3	523	2	T05946	xylian 1,4-beta-xy1	336	75.5	4.3	2109	1	TS0421	hypotheical prote
264	77	4.3	796	2	UC7966	VLDL receptor prec	337	75	4.2	150	2	D95131	probable anthranil
265	77	4.3	873	1	QRRBVD	leukocyte surface	338	75	4.2	208	2	D71529	probable beta-keto
266	77	4.3	1021	2	I39207	probable RND efflu	339	75	4.2	466	2	D84906	glucose-6-phosphat
267	77	4.3	1029	2	D83120	probable membrane	340	75	4.2	491	2	AC2650	glucose-6-phosphat
268	77	4.3	1041	2	S55862	leukocyte antigen-	341	75	4.2	503	2	B97432	glutamate/aspartat
269	77	4.3	1897	1	TDRHUK	cell wall-associat	342	75	4.2	543	2	S26609	Ig Y heavy chain (
270	77	4.3	2167	2	AF1489	herc2 protein - mo	343	75	4.2	572	2	B46529	Ig mu chain precu
271	77	4.3	4836	2	T14346	non-specific cross-	344	75	4.2	573	2	S12838	hypotheical prote
272	76.5	4.3	177	1	C40428	molybdopterin-guan	345	75	4.2	622	2	A55665	glutamate/aspartat
273	76.5	4.3	191	2	E75132	hypotheical prote	346	75	4.2	686	2	B96751	glutamate/aspartat
274	76.5	4.3	238	2	T24314	conserved hypotet	347	75	4.2	747	1	ORCPE	outer membrane rec
275	76.5	4.3	251	2	S75312	hypotheical prote	348	75	4.2	747	2	B85499	outer membrane rec
276	76.5	4.3	266	2	G82131	hypotheical prote	349	75	4.2	747	2	B90648	fibroblast growth
277	76.5	4.3	330	2	D86291	hypotheical prote	350	75	4.2	821	1	TVMSBK	macrophage colony-
278	76.5	4.3	394	2	S20905	pregnancy-specific	351	75	4.2	976	1	TVMSMD	neural cell adhesi
279	76.5	4.3	402	2	AS4312	N-carbamyl-L-amino	352	75	4.2	1091	1	IJCNTL	CDO protein - rat
280	76.5	4.3	433	2	AB1142	pregnancy-specific	353	75	4.2	1256	2	T03096	hypotheical prote
281	76.5	4.3	466	2	S09016	pregnancy-specific	354	75	4.2	1338	2	T02206	elasic ticlin - hu
282	76.5	4.3	466	2	C55181	pregnancy-specific	355	75	4.2	7962	2	I38346	ovalbumin-related
283	76.5	4.3	426	2	B35334	pregnancy-specific	356	74.5	4.2	232	1	DXCH	carcinoembryonic a
284	76.5	4.3	436	2	B55181	pregnancy-specific	357	74.5	4.2	278	2	A339037	hypotheical prote
285	76.5	4.3	495	2	AS5181	pregnancy-specific	358	74.5	4.2	309	2	T31908	hypotheical prote
286	76.5	4.3	497	2	D65189	viGc protein - Esc	359	74.5	4.2	321	2	S10006	lipoprotein D prec
287	76.5	4.3	582	2	A71506	DNA polymerase III	360	74.5	4.2	379	2	B55522	probable lipoprote
288	76.5	4.3	727	2	T23585	hypotheical prote	361	74.5	4.2	379	2	D91078	lipoprotein [impor
289	76.5	4.3	838	2	S17906	hypotheical prote	362	74.5	4.2	379	2	E85923	hypotheical prote
290	76.5	4.3	839	2	B96538	serine/chreonine-s	363	74.5	4.2	463	3	T14884	conserved hypotet
291	76.5	4.3	876	2	S71377	hypotheical prote	364	74.5	4.2	518	2	D69539	protein-tyrosine k
292	76.5	4.3	876	2	D85350	Ig heavy chain - C	365	74.5	4.2	544	2	I51593	tricyclicglycerol 11
293	76.5	4.3	1005	2	T18537	hypotheical prote	366	74.5	4.2	688	2	A47705	fibroblast growth
294	76.5	4.3	1043	2	T119734	suppressor protein	367	74.5	4.2	705	2	S51635	probable transport
295	76.5	4.3	1071	2	T18307	platelet-derived g	368	74.5	4.2	741	2	F907139	irregular chiasm C
296	76.5	4.3	1089	1	PFHUGA	zinc finger protei	369	74.5	4.2	741	2	H85589	hypotheical prote
297	76.5	4.3	1124	2	JX0293	ATP-binding repr	370	74.5	4.2	764	2	A49448	probable membrane
298	76.5	4.3	1154	2	AS6242	probable polyeicid	371	74.5	4.2	771	2	T34376	hypotheical prote
299	76.5	4.3	1328	2	S62467	HKR1 protein precu	372	74.5	4.2	786	2	H64817	hypothetical prote
300	76.5	4.3	1461	2	B70588	ankyrin-related un	373	74.5	4.2	795	2	T20609	hypothetical prote
301	76.5	4.3	1802	2	S69703	photosystem I prot	374	74.5	4.2	884	1	VCLJG5	env polyprotein -
302	76.5	4.3	2039	2	T15347	mannose-specific p	375	74.5	4.2	899	2	T00326	hypothetical prote
303	76	4.3	138	2	S16199	Ig lambda chain -	376	74.5	4.2	1003	2	T19638	glutamate receptor
304	76	4.3	144	2	AH1172	hypotheical prote	377	74.5	4.2	1007	2	PN0156	glutamate receptor
305	76	4.3	230	2	S49449	probable carboxype	378	74.5	4.2	1008	2	S28858	glutamate receptor
306	76	4.3	239	2	T23147	probable carboxype	379	74.5	4.2	1021	2	A57112	contactin precuro
307	76	4.3	262	2	A64882	probable carboxype	380	74.5	4.2	1128	2	E87145	[beta] subunit of
308	76	4.3	262	2	A99867	probable carboxype	381	74.5	4.2	1179	2	S31145	DNA-directed RNA p
309	76	4.3	262	2	H85751	prephenate dehydro	382	74.5	4.2	1522	2	T00028	brain-specific ang
310	76	4.3	286	2	B97010	conserved hypotet	383	74.5	4.2	1723	2	S58880	receptor DRC-205 -
311	76	4.3	305	2	H69759	amalgam protein pr	384	74.5	4.2	1896	2	T08881	Down syndrome cell
312	76	4.3	333	2	A31923	brevican precursor	385	74.5	4.2	2256	2	AD1018	large repetitive p
313	76	4.3	378	1	S55194	DNA-directed DNA p	386	74.5	4.2	2364	2	A56577	microtubule-associ
314	76	4.3	487	1	S55194	DNA-directed DNA p	387	74.5	4.2	2783	2	T34416	hypotheical prote
315	76	4.3	507	2	T47021	hypotheical prote	388	74	4.2	203	3	S36291	T-cell receptor ga
316	76	4.3	508	2	AD0236	L-asparagine perme	389	74	4.2	234	2	S01320	Ig kappa chain pre
317	76	4.3	550	2	G90497	hypotheical prote	390	74	4.2	278	2	UC1506	bilary glycoprote
318	76	4.3	758	2	T11577	hypotheical prote	391	74	4.2	333	2	PS0018	Ig gamma-2b chain
319	76	4.3	841	2	T01011	hypotheical prote	392	74	4.2	334	2	T19637	hypothetical prote
320	76	4.3	964	2	T15746	macrophage colony-	393	74	4.2	349	2	S68092	protein-glutamine
321	76	4.3	978	2	S16385		394	74	4.2	384	2	H64161	hypotheical prote

395	74	4.2	403	2	I52590	m3-B isoform - mo	468	72.5	4.1	202	2	S36293	T-cell receptor ga
396	74	4.2	424	2	T43498	hypothetical prote	469	72.5	4.1	221	2	T31620	hypothetical prote
397	74	4.2	463	2	C69997	probable prolina t	470	72.5	4.1	334	2	G01650	malate dehydrogena
398	74	4.2	468	2	S70297	SPS2 protein homol	471	72.5	4.1	336	2	C27658	pregnancy-specific
399	74	4.2	502	2	T40792	hypothetical prote	472	72.5	4.1	342	2	AG1729	protein gp19 (Bact
400	74	4.2	548	2	A44302	protein-glutamine	473	72.5	4.1	351	2	B34595	pregnancy-specific
401	74	4.2	586	2	T15259	hypothetical prote	474	72.5	4.1	363	2	T19726	mannopine biosynth
402	74	4.2	611	2	P82442	probable peptide A	475	72.5	4.1	371	2	T40287	hypothetical prote
403	74	4.2	645	2	T39614	kinase-binding pro	476	72.5	4.1	377	2	B90437	hypothetical prote
404	74	4.2	673	2	T48701	hypothetical prote	477	72.5	4.1	399	2	A11114	surface protein (p
405	74	4.2	860	2	UC5702	ErbB kinase activa	478	72.5	4.1	424	2	A34595	pregnancy-specific
406	74	4.2	862	2	I49583	differentiation an	479	72.5	4.1	435	2	D33258	pregnancy-specific
407	74	4.2	876	2	B96993	probable receptor	480	72.5	4.1	440	2	S52895	TyA protein - yea
408	74	4.2	900	2	G96617	probable disease r	481	72.5	4.1	443	2	AE3294	colB protein limpo
409	74	4.2	1063	2	A33830	cation efflux syat	482	72.5	4.1	478	2	AA9228	trypsin-like prote
410	74	4.2	1063	2	JC4700	cadmium, zinc, cob	483	72.5	4.1	487	2	A11146	hypothetical cell
411	74	4.2	1130	2	T23104	hypothetical prote	484	72.5	4.1	491	2	T22844	hypothetical prote
412	74	4.2	1133	2	T23103	hypothetical prote	485	72.5	4.1	527	2	D75127	hypothetical prote
413	74	4.2	1165	1	S45879	chitin synthase (B	486	72.5	4.1	666	2	A39610	SLY1 protein - yea
414	74	4.2	1237	2	E86457	probable RNA helic	487	72.5	4.1	682	2	A35969	heparin-binding gr
415	74	4.2	1367	2	T33819	hypothetical prote	488	72.5	4.1	687	2	T39838	hypothetical prote
416	74	4.2	1582	2	T15308	hypothetical prote	489	72.5	4.1	768	2	UC7352	glucose-regulated
417	74	4.2	4344	1	AS3489	dyslin heavy chain	490	72.5	4.1	769	2	T45854	hypothetical prote
418	74	4.2	5232	2	A45086	HC-toxin synthetas	491	72.5	4.1	842	2	E96641	hypothetical prote
419	74	4.2	6658	2	T13931	proteoglycan - frut	492	72.5	4.1	851	2	S44890	nc1-1 ZK112.2 prot
420	73.5	4.1	325	2	S49451	cysteine proteins	493	72.5	4.1	876	2	A49508	protein-tyrosine k
421	73.5	4.1	364	2	A30521	myleoid cell surfa	494	72.5	4.1	895	2	T11976	proprotein translo
422	73.5	4.1	428	2	B83967	dihydroorotase pyr	495	72.5	4.1	913	2	A48280	receptor tyrosine
423	73.5	4.1	647	2	T33773	hypothetical prote	496	72.5	4.1	1057	2	S45801	probable membrane
424	73.5	4.1	740	2	AH0600	probable membrane	497	72.5	4.1	1123	2	AB0125	exodeoxyribonuclea
425	73.5	4.1	797	2	T27518	hypothetical prote	498	72.5	4.1	1138	2	A82939	neurofascin - chic
426	73.5	4.1	850	2	JC5700	ErbB kinase activa	499	72.5	4.1	1272	2	S26180	transmembrane prot
427	73.5	4.1	880	1	VCLJ32	env polypeptid pr	500	72.5	4.1	1434	2	T10172	lysobactin synthet
428	73.5	4.1	923	2	P84732	probable ligand ga	501	72.5	4.1	1575	2	T18545	dynein heavy chain
429	73.5	4.1	926	2	D83888	glucan 1,4-beta-gl	502	72.5	4.1	4367	1	B54802	probable peptide s
430	73.5	4.1	957	2	C69463	type I restriction	503	72.5	4.1	4924	2	T50176	hypothetical prote
431	73.5	4.1	1166	2	S37692	probable tumor sup	504	72.5	4.1	4936	2	AH2515	purine nucleoside
432	73.5	4.1	1225	2	T48251	ubiquitin-protein	505	72.5	4.1	265	2	H72233	hypothetical prote
433	73.5	4.1	1240	2	T03097	CDO protein - huma	506	72.5	4.1	320	2	C89867	scarcrow-like pro
434	73.5	4.1	2013	2	AD1129	probable peptidogl	507	72.5	4.1	378	2	T51237	hypothetical prote
435	73.5	4.1	2042	2	TI8359	variant-specific s	508	72.5	4.1	423	2	T25349	hypothetical prote
436	73.5	4.1	2301	1	GNNYTN	genome polypeptid	509	72.5	4.1	437	2	AF3613	hypothetical prote
437	73.5	4.1	3255	2	G81702	adherence factor T	510	72.5	4.1	442	2	E71523	hypothetical prote
438	73.5	4.1	4544	1	S02392	alpha-2-macroglobu	511	72.5	4.1	446	2	B89922	conserved hypothet
439	73.5	4.1	147	2	T34265	hypothetical prote	512	72.5	4.1	469	2	C69628	gamma-aminobutylat
440	73.5	4.1	220	1	G69047	conserved hypothet	513	72.5	4.1	506	2	F69867	two-component sens
441	73.5	4.1	235	1	S14675	Ig lambda chain -	514	72.5	4.1	510	2	A84707	probable pseudouri
442	73.5	4.1	250	2	S27544	hypothetical prote	515	72.5	4.1	521	2	E82377	ABC transporter, p
443	73.5	4.1	293	2	H96906	hypothetical prote	516	72.5	4.1	543	2	S38353	glutamate transp
444	73.5	4.1	322	2	H84095	hypothetical prote	517	72.5	4.1	549	2	T33517	hypothetical prote
445	73.5	4.1	354	2	T22712	hypothetical prote	518	72.5	4.1	558	2	T01343	hypothetical prote
446	73.5	4.1	389	2	T46722	conserved hypothet	519	72.5	4.1	565	2	C82280	sensor kinase cItA
447	73.5	4.1	397	2	E86504	Fc11.9 protein - A	520	72.5	4.1	589	2	S48929	hypothetical prote
448	73.5	4.1	413	2	S65948	hemolin - A	521	72.5	4.1	595	2	T16774	hypothetical prote
449	73.5	4.1	432	1	A37778	hemolin - cecropia	522	72.5	4.1	617	2	T23197	hypothetical prote
450	73.5	4.1	433	1	RMNQT4	T-cell surface glyco	523	72.5	4.1	646	2	I38049	cell surface glyco
451	73.5	4.1	476	2	H84524	probable fatty aci	524	72.5	4.1	783	2	T45899	receptor protein k
452	73.5	4.1	519	2	S38921	hypothetical prote	525	72.5	4.1	808	2	F81180	conserved hypothet
453	73.5	4.1	590	2	I56526	interleukin 1 rece	526	72.5	4.1	868	2	UC5701	ErbB kinase activa
454	73.5	4.1	666	1	A36026	kinasin-related pr	527	72.5	4.1	873	2	H96503	protein Pg16.17 (
455	73.5	4.1	730	2	S64998	hypothetical prote	528	72.5	4.1	885	2	D86151	F22M8.8 protein -
456	73.5	4.1	735	2	T00850	probable receptor-	529	72.5	4.1	900	2	T04839	protein kinase hom
457	73.5	4.1	853	1	IJBONC	neural cell adhesi	530	72.5	4.1	901	2	S07445	core protein p3 -
458	73.5	4.1	864	2	JH0438	penicillin-binding	531	72.5	4.1	911	2	B34721	androgen receptor
459	73.5	4.1	901	1	P3XR17	core protein VP3 -	532	72.5	4.1	1038	2	H90053	hypothetical prote
460	73.5	4.1	1014	2	T13476	hypothetical prote	533	72.5	4.1	1186	2	T19334	hypothetical prote
461	73.5	4.1	1072	2	A38457	integrin alpha-6 c	534	72.5	4.1	1214	2	JC7259	Smad interacting p
462	73.5	4.1	1171	2	T31635	hypothetical prote	535	72.5	4.1	1216	2	H85023	hypothetical prote
463	73.5	4.1	1179	2	T05673	hypothetical prote	536	72.5	4.1	1273	2	T42405	sax-3 protein - Ca
464	73.5	4.1	1515	1	S51863	cadmium resistance	537	72.5	4.1	1348	2	S51656	vascular endotheli
465	73.5	4.1	1737	1	AS9235	unconventional myo	538	72.5	4.1	1906	1	S68235	myosin-light-chain
466	73.5	4.1	1806	2	T23298	hypothetical prote	539	72.5	4.1	2383	2	D64962	probable membrane
467	73.5	4.1	3788	2	T30851	lysosomal traffick	540	72.5	4.1	4872	2	S27272	ryanodine receptor

541	71.5	4.0	145	2	S25743	Ig lambda chain	614	71	4.0	1251	2	T21389	hypothetical prote
542	71.5	4.0	229	1	B43685	nonstructural prot	615	71	4.0	1338	2	S09982	protein-tyrosine k
543	71.5	4.0	238	2	A49633	Ig lambda-like cha	616	71	4.0	4391	2	A38096	perlecan precursor
544	71.5	4.0	299	2	S50803	hypothetical prote	617	71	4.0	5107	2	T29144	partial CDS - Caen
545	71.5	4.0	312	2	A64461	hypothetical prote	618	70.5	4.0	203	3	F69381	flagellin (flaB1-1
546	71.5	4.0	338	2	A64303	conserved hypoch	619	70.5	4.0	223	2	A81068	hypothetical prote
547	71.5	4.0	339	2	S08981	malate dehydrogena	620	70.5	4.0	238	2	D86302	hypothetical prote
548	71.5	4.0	362	2	T05167	hypothetical prote	621	70.5	4.0	246	2	B82764	hypothetical prote
549	71.5	4.0	443	2	T14916	mitosis-specific c	622	70.5	4.0	332	2	T45770	hypothetical prote
550	71.5	4.0	498	2	G90067	malate quinone oxi	623	70.5	4.0	338	1	DERTM	malate dehydrogena
551	71.5	4.0	500	2	T11946	ribosomal protein	624	70.5	4.0	358	1	E89588	protein R09F10.8 l
552	71.5	4.0	542	2	AF2587	MPS permease limpo	625	70.5	4.0	429	1	B41902	arsenical pump mem
553	71.5	4.0	542	2	F97369	hypothetical prote	626	70.5	4.0	455	2	G01923	KIR (GL-5) NK rece
554	71.5	4.0	589	2	T50385	hypothetical coile	627	70.5	4.0	502	2	T19108	hypothetical prote
555	71.5	4.0	603	2	H84442	hypothetical prote	628	70.5	4.0	505	2	T15159	hypothetical prote
556	71.5	4.0	669	2	T48466	hypothetical prote	629	70.5	4.0	522	2	T26319	hypothetical prote
557	71.5	4.0	707	2	A54846	fibroblast growth	630	70.5	4.0	526	1	TFV60	protein-tyrosine k
558	71.5	4.0	707	2	A38429	keratinocyte growth	631	70.5	4.0	533	1	TVCHS	protein-tyrosine k
559	71.5	4.0	764	1	QRHUCS	secretory componen	632	70.5	4.0	537	1	A45501	protein-tyrosine k
560	71.5	4.0	822	2	BS4846	fibroblast growth	633	70.5	4.0	545	2	S52313	protein-tyrosine k
561	71.5	4.0	919	2	S33942	hexon protein - hu	634	70.5	4.0	546	2	S52314	protein-tyrosine k
562	71.5	4.0	921	2	F71486	probable yopC/gen	635	70.5	4.0	557	1	TFV52	protein-tyrosine k
563	71.5	4.0	1032	2	H64100	acridiflavine resist	636	70.5	4.0	558	1	MMXRT	RNA 10 protein - r
564	71.5	4.0	1089	1	S33727	platelet-derived g	637	70.5	4.0	568	1	TFVFS1	protein-tyrosine k
565	71.5	4.0	1180	2	E86719	hypothetical prote	638	70.5	4.0	569	2	A45624	leprohoroite cystei
566	71.5	4.0	1348	2	S27812	probable epidermal	639	70.5	4.0	587	1	TVFVPR	protein-tyrosine k
567	71.5	4.0	1348	2	A43917	probable epidermal	640	70.5	4.0	627	2	G14683	Ig mu chain precur
568	71.5	4.0	1374	2	S62524	probable RNA helic	641	70.5	4.0	627	2	A69663	DNA mismatch repai
569	71.5	4.0	1377	2	C70148	DNA-directed RNA p	642	70.5	4.0	630	2	A39344	tumor-associated m
570	71.5	4.0	1413	2	D84481	probable retroelem	643	70.5	4.0	646	2	T48644	negative regulator
571	71.5	4.0	1462	2	T11648	probable mitotic s	644	70.5	4.0	656	2	H84206	acetyl-CoA synthet
572	71.5	4.0	2397	1	A55535	versican precursor	645	70.5	4.0	663	1	TVWVRR	protein-tyrosine k
573	71.5	4.0	61	2	C82536	hypothetical prote	646	70.5	4.0	669	2	T13640	probable minor str
574	71.5	4.0	142	2	S38392	T-cell receptor be	647	70.5	4.0	783	2	F71062	hypothetical prote
575	71.5	4.0	189	2	G64496	hypothetical prote	648	70.5	4.0	747	2	T41974	replication origin
576	71.5	4.0	207	2	T50206	hypothetical zinc	649	70.5	4.0	793	2	T41703	dipeptidyl aminope
577	71.5	4.0	221	2	T21117	hypothetical prote	650	70.5	4.0	844	2	S05988	translacion elonga
578	71.5	4.0	224	2	H81568	conserved hypoch	651	70.5	4.0	877	1	IJBOCN	N-cadherin precurs
579	71.5	4.0	231	2	G72102	ct181 hypothetical	652	70.5	4.0	878	2	S11842	hypothetical prote
580	71.5	4.0	231	2	B86520	ct181 hypothetical	653	70.5	4.0	895	2	A55413	triglyceride trans
581	71.5	4.0	258	2	S73803	MC256 homolog H91	654	70.5	4.0	906	1	IJMSCN	N-cadherin precurs
582	71.5	4.0	329	1	DEDFLM	L-lactate dehydrog	655	70.5	4.0	928	2	G86546	polymorphic outcr
583	71.5	4.0	333	2	AP0407	lipoprotein limpor	656	70.5	4.0	928	2	G81591	polymorphic membra
584	71.5	4.0	343	2	A10358	probable fibrinial	657	70.5	4.0	938	2	P86548	polymorphic outcr
585	71.5	4.0	344	2	I56551	neurotrophin - rat	658	70.5	4.0	938	2	H72074	polymorphic membra
586	71.5	4.0	345	2	I48780	Stral/Epig2 protei	659	70.5	4.0	1088	2	B56715	calcium receptor (
587	71.5	4.0	346	2	AF1820	straloglycoproteina	660	70.5	4.0	1200	2	T17404	hyalinn - sea urchi
588	71.5	4.0	387	2	B71611	ubiquitinol-cytochro	661	70.5	4.0	1356	2	JC1402	protein-tyrosine k
589	71.5	4.0	389	2	S68155	hypothetical prote	662	70.5	4.0	1402	2	P84480	probable retroelem
590	71.5	4.0	390	2	T27033	hypothetical prote	663	70.5	4.0	1427	2	I51669	tumor suppressor -
591	71.5	4.0	407	2	T34442	hypothetical prote	664	70.5	4.0	1654	2	S50065	receptor tyrosine
592	71.5	4.0	423	1	EHMS	Ig epsilon chain C	665	70.5	4.0	2051	2	T30938	receptor tyrosine
593	71.5	4.0	455	2	S50391	drought-inducible	666	70.5	4.0	2303	1	GNNYTP	genome polyprotein
594	71.5	4.0	462	2	JN0719	amino acid transpo	667	70.5	4.0	2303	1	S13554	microtubule-associ
595	71.5	4.0	463	2	AH1758	Mg-R protein - myx	668	70.5	4.0	2464	1	ORMSPI	protein unc-22 (im
596	71.5	4.0	509	1	MMVZMX	probable pyruvate	669	70.5	4.0	6831	2	A88852	twitchein (similari
597	71.5	4.0	570	2	T11647	GTP-binding protei	670	70.5	4.0	6839	2	S57242	Ig kappa chain pre
598	71.5	4.0	609	2	H82039	glucanase 2-dehydr	671	70.5	4.0	7160	2	T27935	T-cell receptor ga
599	71.5	4.0	615	2	B38575	soluble vascular e	672	70.5	4.0	115	1	KVMSL6	CMRF-35 antigen -
600	71.5	4.0	682	2	T22064	triacylglycerol 11	673	70.5	4.0	203	2	S23043	Ig lambda chain -
601	71.5	4.0	687	2	A49636	glycerol ester hyd	674	70.5	4.0	224	2	I37243	probable maltodex
602	71.5	4.0	690	2	A24545	hypothetical prote	675	70.5	4.0	226	2	S25746	hypothetical prote
603	71.5	4.0	691	2	B89797	fibroblast growth	676	70.5	4.0	283	2	AB0105	probable binding p
604	71.5	4.0	765	2	E96558	WD40-repeat protei	677	70.5	4.0	292	2	T44230	protein-tyrosine k
605	71.5	4.0	821	1	TVHUP2	probable carrier p	678	70.5	4.0	309	2	D83010	hemin transport sy
606	71.5	4.0	876	2	T51507	hypothetical prote	679	70.5	4.0	347	2	T29415	ORF1 protein - Chl
607	71.5	4.0	902	2	S54495	isolectin-CRMA 11	680	70.5	4.0	356	2	G82838	serine proteinase
608	71.5	4.0	940	2	T41992	hypothetical prote	681	70.5	4.0	374	2	A46352	hypothetical prote
609	71.5	4.0	956	2	G70327	receptor protein k	682	70.5	4.0	403	2	B36151	hypothetical prote
610	71.5	4.0	1018	2	A54744	regulatory protein	683	70.5	4.0	410	2	I50494	hypothetical prote
611	71.5	4.0	1027	2	B85089	hypothetical prote	684	70.5	4.0	469	2	T46929	
612	71.5	4.0	1082	2	S64903		685	70.5	4.0	491	2	T27661	
613	71.5	4.0	1217	2	T22672		686	70.5	4.0	491	2	T27661	

```

687 70 4.0 517 2 T00980 hypothetical prote
688 70 4.0 536 2 T37544 hypothetical serin
689 70 4.0 548 2 B71549 hypothetical prote
690 70 4.0 550 2 T03714 5-epi-aristoloch
691 70 4.0 576 2 A32604 interleukin-1 rece
692 70 4.0 599 2 T48450 hypothetical prote
693 70 4.0 609 2 AE2062 gamma-glutamyltran
694 70 4.0 611 1 W1WLEP E1 protein - Europ
695 70 4.0 611 2 H70938 probable fads pro
696 70 4.0 648 2 T08856 hypothetical prote
697 70 4.0 687 1 A39045 protein-glutamine
698 70 4.0 790 2 T01537 s-receptor kinase
699 70 4.0 805 2 S68441 lepton receptor, s
700 70 4.0 810 1 S57196 calpain (EC 3.4.22

```

## ALIGNMENTS

## RESULT 1

Ly-9.2 antigen - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C:Accession: A46500  
 R:Sandrin, M.S.; Gunley, T.P.; Henning, M.M.; Vaughan, H.A.; Genez, L.J.; Trapani, J.A.;  
 J. Immunol. 149, 1636-1641, 1992  
 A:Title: Isolation and characterization of cDNA clones for mouse Ly-9.  
 A:Reference number: A46500; MUID:92373005; PMID:1506686  
 A:Accession: A46500  
 A:Status: preliminary  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-629 <SAN>  
 A:Cross-references: GB:M84412; NID:g198931; PIDN:AAA39468.1; PID:g198932  
 A:Experimental source: C57BL/6  
 A:Note: Sequence extracted from NCBI backbone (NCBIN:111651, NCBIPI:111654)  
 C:Keywords: transmembrane protein

Query Match 19.4%; Score 343; DB 2; Length 629;  
 Best Local Similarity 29.3%; Pred. No. 2.2e-20;

Matches 105; Conservative 58; Mismatches 143; Indels 52; Gaps 14;

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QY 14 LMQL-TGSA-----ASGPVKELVSGAATFPLKSK-VKQVDSIYVTFNTPLVITIQPEG 67
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 217 IMQFCTGAGRRKTAAG--KTVVGILGEPTVLPLEFPAATATKVVAVLMTS--VISQERR 272
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 68 GTIITVQNR-----NREYDFPDGYSGLSKLKKKNDGIIYVGIYSSLSQPSIOEYVL 122
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 273 GAATADSRKRPKSGEERVRVTSDDQSLKISQLKMEADAPYAHAYVCSASRDPVSVAHFTL 332
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 123 HYVEHLKRPKVTMGLQSNKNGTCVTNLTCMEHGEEDVITYWKAALQANESHNGSLPI 182
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 333 LYYKLEKESVTKSPYHMMANGICEVVLTCSDGKNVYITWMLPNKAKVMGCGSHLNV 392
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 183 SWRMGSDMTFICVARNPVSRNFPSSDILARKLCEGAADPDSDSVLLCLLVPLLSLTFV 242
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 393 SWESGEHLNPFCTANPVS--NSSSQFSSGTCISG-----PENRKRWMLLLLVLLMLMI 447
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 243 LGLFLMFLKROEELIEEK-KRVIDICRETPNICPSG-----ENTPE 283
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 448 GGYFFI-LRKKKQCSLARRRAEPAEIPR--PPTGQGPSVLGQRYEKLDMSAKTRP 503
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 284 Y-----DTIPHTNRILLKEDPANTYSTVEIPKKMENHSLILTMPDTRLPAYEVNI 335
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 504 HQTPTSDTSSSSATTEEDDEKTRMHSIANSRNQL---YDLVTHODIAHALAYEGQV 558
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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## RESULT 2

S58892  
 signaling lymphocytic activation molecule - human  
 C:Species: Homo sapiens (man)  
 C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 05-Nov-1999  
 C:Accession: S58892

R:Cocks, B.G.; Chang, C.C.; Cardallido, J.M.; Yssel, H.; de Vries, J.E.; Aversa, G.  
 Nature 376, 260-263, 1995  
 A:Title: A novel receptor involved in T-cell activation.  
 A:Reference number: S58892; MUID:95342241; PMID:7617038  
 A:Accession: S58892  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-335 <COC>  
 A:Cross-references: EMBL:U33017; NID:g984968; PIDN:AAV5380.1; PID:g984969

Query Match 10.3%; Score 182.5; DB 2; Length 335;  
 Best Local Similarity 22.5%; Pred. No. 1.9e-07;

Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

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QY 8 LFLIYILW-QLTGSASGP-----VKELVSGAATFPL-----SKYKQVDSIYWT 54
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 7 LSLRVLFLSLAFGASYSYTGGRMNCPIKLKQLGSKVLLPLYTERINKSNKSHIIVTM 66
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 55 FNT-----TPLYTIQ-EGGTIIIVTONRNERVDFPDGYSGLSKLKKKNDGIIYVGI 107
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 67 AKSLNSVENKIVSLDPEAG-----PPRYLDGRYKFFYLENLTLGIRSRKDEGMYLMTL 122
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 108 YSS-SLQQPSIOEYVLHYVEHLKRPKVTMGLQSNKNGTCVTNLTCMEHGEEDVITYW-- 164
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 123 EKQVSVQRFCLQ---LRLVEQVSTPEIKVLMKTOENGCTTILGCTVEKGDH-VAYSWS 178
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 165 KALGAANESHNGSLPIPSWMEGSDMTFICVARNPVSRNFS--SPILARKLCEGAADP 222
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 179 KAGTHPLPNPANSHLISLILGPOHADNITIVCSNPISNQSOTSP-----WPCRTRDP 232
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 223 DSSM-----VLLCLLVPLLSLFLVGLFLMKEROREEYIE---EKKRVDC 268
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 223 SETKPMAYVAGLLGCVIMILIMVILQ-----LRRGKNVHYQTVEKSLCTIY 281
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 269 RETPNICHSGENTEYDTIPHTNRILLKEDPANTY--STVEIPKKMENPMSL-----LT 321
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 282 AQVQKRP---LQKRLDSFP-----AQDPCTIIVYATEPVPSPVOETNSITVYASVT 331
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 322 MPDT 325
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 332 LPES 335
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

## RESULT 3

B28967  
 T-cell surface glycoprotein CD2 precursor - mouse  
 M:Alternate names: CD2 antigen; T-lymphocyte antigen CD2; T11 protein  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1989 #sequence\_revision 03-Jun-1993 #text\_change 23-Jul-1999  
 C:Accession: B28967; S01347; S02293  
 R:Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988  
 A:Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)  
 A:Reference number: A28967; MUID:86144486; PMID:2894031  
 A:Accession: B28967  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <DIA>  
 A:Cross-references: GB:M19807; NID:g192479; PIDN:AAA37393.1; PID:g387122; GB:J03622; GB:..  
 A:Note: The authors translated the codon TAT for residue 99 as Thr  
 R:Clayton, L.K.; Sayre, P.H.; Novotny, J.; Reinherz, E.L.  
 Eur. J. Immunol. 17, 1367-1370, 1987  
 A:Title: Murine and human T11 (CD2) cDNA sequences suggest a common signal transduction  
 A:Reference number: S01347; MUID:88004738; PMID:2820751  
 A:Accession: S01347  
 A:Molecule type: mRNA  
 A:Residues: 1-127, 'M', 129-174, 'N', 176-190, 'NM', 193-344 <CIA>  
 A:Cross-references: EMBL:X06143; NID:G54223; PIDN:CAA29500.1; PID:G54224  
 R:Seewell, M.A.; Brown, M.H.; Owen, M.J.; Fink, P.J.; Kozak, C.A.; Crumpton, M.J.  
 Eur. J. Immunol. 17, 1015-1020, 1987  
 A:Title: The murine homologue of the T lymphocyte CD2 antigen: molecular cloning, chromo  
 A:Reference number: S02293; MUID:87276135; PMID:2440689  
 A:Accession: S02293  
 A:Status: not compared with conceptual translation

A.Molecule type: mRNA  
 A.Residues: 1-127,'M',129-174,'N',176-191,'M',193-344 <SEM>  
 A.Cross-References: EMBL:Y00023; NID:G50346; PIDD:CAA68258.1; PID:G50347  
 C.Genetic: 8  
 A:Map position: 3  
 C:Superfamily: T-cell surface glycoprotein CD2  
 C:Keywords: glycoprotein; surface antigen; T-cell; transmembrane protein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:23-34/Domain: T-cell surface glycoprotein CD2 #status predicted <MAT>  
 F:23-34/Domain: extracellular #status predicted <EXT>  
 F:204-228/Domain: transmembrane #status predicted <TM>  
 F:229-344/Domain: intracellular #status predicted <INT>

Query Match 8.1%; Score 144; DB 2; Length 344;  
 Best Local Similarity 21.4%; Pred. No. 0.0003;

Matches 72; Conservative 56; Mismatches 132; Indels 76; Gaps 16;

QY 12 YILMOLTGSAGSPVKELV-GSVGAVT--FPLKSKYKQVDSIVMTFNTTPLVTIQPEGG 68  
 ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 10 FILFSLSGKAGDCRDNBTWGVGHGTTINIPFQMTDIDDEVKVV-----RRG 58  
 QY 69 TIIIVTGNRR-----ERVDPDGGYSLKLSK-LKKNDSGIYVGYSSSLQOPSTQEVY 121  
 ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 59 TIVAEFRKKRPPLISETYEVLANG-SLKIKKPMENNDGTYVWVYGTGKMTREKDD 117  
 QY 122 LHVYEHLSRPKVTMGLOSNKNGTCV-TNLTCCHEHEEDVIYTWKALGQANESHNGSIL 180  
 ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 118 VILERSVSKPVI-----HMECPNTTLTCAVLQGTDELEKLYQ--GETLINS-----L 162  
 QY 181 P--ISMRKGESEDMFTICVARNPVSRNFSPLIARLKEGADDPSSSVNLCL----- 231  
 ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 163 PQKNMSYQWNTNLSAPKCEAINPVSKESKTEVV-----NCEPKGJSPYTVGVGAG 213  
 QY 232 -LLVPLLSLFLVGLFPLMFLKREOREYIEKKRVDCRETPNICPHSGENTYDTPHPT 290  
 ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 214 GLLVLVLVLF--FCICRRKRNRRRRDELEIKASRTS-----TYERGKPHS 261  
 QY 291 NRTILKEDPANTVYSTEIVPKKEMPHSLTMDTP 326  
 ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 262 T-----PAAAQNSVALQAPPPGHHLOTGHRP 290

## RESULT 4

149585  
 CD2 antigen protein precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #ext\_change 23-Jul-1999  
 C:Accession: I49585  
 R.Yagita, H.; Okumura, K.; Nakachi, H.  
 J. Immunol. 140, 1321-1326, 1988  
 A>Title: Molecular cloning of the murine homologue of CD2: Homology of the molecule to  
 A:Reference number: I49585; MUID:88140313; PMID:3257775  
 A:Accession: I49585  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <RES>  
 A.Cross-References: GB:M18934; NID:G192486; PIDD:AAA37397.1; PID:G309158  
 C:Superfamily: T-cell surface glycoprotein CD2

Query Match 7.8%; Score 138; DB 2; Length 344;  
 Best Local Similarity 21.1%; Pred. No. 0.00095;

Matches 71; Conservative 56; Mismatches 133; Indels 76; Gaps 16;

QY 12 YILMOLTGSAGSPVKELV-GSVGAVT--FPLKSKYKQVDSIVMTFNTTPLVTIQPEGG 68  
 ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 10 FILFSLSGKAGDCRDNBTWGVGHGTTINIPFQMTDIDDEVKVV-----RRG 58  
 QY 69 TIIIVTGNRR-----ERVDPDGGYSLKLSK-LKKNDSGIYVGYSSSLQOPSTQEVY 121  
 ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 59 TIVAEFRKKRPPLISETYEVLANG-SLKIKKPMENNDGTYVWVYGTGKMTREKDD 117  
 QY 122 LHVYEHLSRPKVTMGLOSNKNGTCV-TNLTCCHEHEEDVIYTWKALGQANESHNGSIL 180  
 ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

DB 118 VILERSVSKPVI-----HMECPNTTLTCAVLQGTDELEKLYQ--GETLINS-----L 162  
 QY 181 P--ISMRKGESEDMFTICVARNPVSRNFSPLIARLKEGADDPSSSVNLCL----- 231  
 ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 163 PQKNMSYQWNTNLSAPKCEAINPVSKESKTEVV-----NCEPKGJSPYTVGVGAG 213  
 QY 232 -LLVPLLSLFLVGLFPLMFLKREOREYIEKKRVDCRETPNICPHSGENTYDTPHPT 290  
 ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 214 GLLVLVLVLF--FCICRRKRNRRRRDELEIKASRTS-----TYERGKPHS 261  
 QY 291 NRTILKEDPANTVYSTEIVPKKEMPHSLTMDTP 326  
 ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
 DB 262 T-----PAAAQNSVALQAPPPGHHLOTGHRP 290

## RESULT 5

RHNC2  
 T-cell surface glycoprotein CD2 precursor - human

N:Alternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #ext\_change 22-Jun-1999  
 C:Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A28874  
 R.Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988  
 A>Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)  
 A:Reference number: A28967; MUID:88144486; PMID:2894031

A:Accession: A28967  
 A:Molecule type: DNA

A:Residues: 1-351 <DNA>

A:Cross-References: GB:J03622; GB:J03623; NID:G180079; PIDD:AAA53095.1; PID:J

R.Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.

Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986

A>Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.

A:Reference number: A26486; MUID:87041523; PMID:2490670.

A:Accession: A26486  
 A:Molecule type: mRNA

A:Residues: 1-338,'M',340,'Q'QKTHCPPLIKKDRNCLPQ' <SE1>

A:Accession: B26486  
 A:Molecule type: protein

A:Residues: 25-46,'X',50 <SE2>

R.Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987

A:Reference number: A28416  
 A:Accession: A28416

A:Contents: revision

A:Accession: A28416

A:Molecule type: mRNA

A:Residues: 333-351 <SE3>

R.Seed, B.; Aruffo, A.

Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987

A>Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rel

A:Reference number: A28023; MUID:87204137; PMID:2437578

A:Accession: A28023

A:Molecule type: mRNA

A:Residues: 1-265,'Q',267-351 <SEB>

A:Cross-References: GB:M16445; NID:G178668; PIDD:AAA51738.1; PID:G178669

R.Sayre, P.H.; Chang, H.C.; Huseby, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C

Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987

A>Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure

A:Reference number: S02292; MUID:87204243; PMID:2883656

A:Accession: S02292

A:Molecule type: mRNA

A:Residues: 1-338,'M',340,'Q'QKTHCPPLIKKDRNCLPQ' <SA1>

A:Cross-References: GB:M16336; NID:G180093; PIDD:AAA51946.1; PID:G180094

A:Accession: A30430

A:Molecule type: protein

A:Residues: 25-43,152-163 <SA2>

R.Liang, G.; Motson, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M.

EMBO J. 7, 1675-1682, 1988

A>Title: The structure of the human CD2 gene and its expression in transgenic mice.

A:Reference number: S00829; MUID:89005055; PMID:2901953

A:Accession: S00829

A:Molecule type: DNA

A:Residues: 1-351 <LAN>

[illegible]

```

Db      71 GKTVEFSSVFEDKRDVLDKTKMGALRIYVNSXSDRGDDIYMRKLHTEBDQ--WKITMEVYDL 127
Oy      128 LSKPKVTMGLQSNKNGTCVTNLTCMEHGSEDIYTYMKALGOANESHGSIIPISWRWG 187
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      128 VSKDAIKIEKTKNLTDSCHLRLSCKVE--DQGVDTWYEDSGPFGQNPGVLEITTPH 185
Oy      188 ESDMTFCIVARNPV 202
       :|||
Db      186 NKSTFYTCQVSNPV 200

RESULT 7
RNRRC2
T-cell surface glycoprotein CD2 precursor - rat
N.Alternate names: CD2 antigen; OX-34 antigen
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text_change 25-Oct-1996
C.Accession: A33071; B27560; A27560; A32346
R.Barclay, A.N.; Williams, A.P.
Submitted to the EMBL Data Library, May 1987
A.Reference number: A33071
A.Accession: A33071
A.Molecule type: mRNA
A.Residues: 1-344 <BAR>
R.Williams, A.P.; Barclay, A.N.; Clark, S.J.; Paterson, D.J.; Willis, A.C.
J. Exp. Med. 165, 368-380, 1987
A.Title: Similarities in sequences and cellular expression between rat CD2 and CD4 antigens
A.Reference number: A27560; MUID:87139793; PMID:3102667
A.Accession: B27560
A.Molecule type: protein
A.Residues: 'X',24-52,'X',54-55,'X',57-62;93-109,119-150,238-245 <MI>
A.Accession: A27560
A.Molecule type: mRNA
A.Residues: 44-344 <MI2>
A>Note: 112-Asn was also found
R.He, Q.; Beyers, A.D.; Barclay, A.N.; Williams, A.F.
Cell 54, 979-984, 1988
A>Title: A role in transmembrane signaling for the cytoplasmic domain of the CD2 T lymphocyte surface glycoprotein
A.Reference number: A32346; MUID:88327862; PMID:2901293
A.Accession: A32346
A.Molecule type: mRNA
A.Residues: 1-33,'H',35-41 <HE1>
A.Cross-references: GB:X05111
C.Superfamily: T-cell surface glycoprotein CD2
C.Keywords: glycoprotein; T-cell; transmembrane protein
F.1-22/Domain: signal sequence #status predicted <SIG>
F.23-34/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F.23-199/Domain: extracellular #status predicted <EXT>
F.200-228/Domain: transmembrane #status predicted <TM>
F.229-344/Domain: intracellular #status predicted <INT>
F.99,106,134/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match          7.3%; Score 130; DB 1; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0044;
Matches    65; Conservative   51; Mismatches 112; Indels 62; Gaps 13;

Oy      12 YIIQLTGSA-----SGPVKELYSVGAATPFPLSKVKQVDISWTFTNTPLVTIQPEG 67
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      10 FLFLSLSKSKADCRDSTVGALGR-GINININFPQMTDIDVR-----ER 56
Oy      68 GTTIIVTONRRERVDPDGYY-----SLKSLKLNKDSGIYVGYSSSLQPSIOEYV 121
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      57 GSTLVAFPEKKRKRPFLKSAGFAELLANGDLIKILTRDSDGTAVTVYSTGWTRILDALD 116
Oy      122 LHAYEHLSKRKYTMGLQSNKNGTCV---TNLTCMEHGSEDIYTYMKALGOANESHG 177
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      117 LRILEWSKSMIWIWEC-SNAITLTCEVLGEIDVELKIYQGEKH-----RSLRQRT----- 165
Oy      178 SLIPSRWGESDMTFICVARNPVSIRNFSPILARKLCBGAAPDPDSWVLLCLLYVL- 236
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      ..66 ----MSIQMNLAAPFKCAVNRYSQSEMEVV-----NCPEGLDLYLIIVGSAG 212
Oy      237 -LISLFPLGLFWFL-----KRROEEYIEEK-KRVDICRETPNICPHS 278

```



Db 213 GULLVFGLFIFCICKRKKRNRRKGELIKASMSYTERGPK--PHS 260

## RESULT 8

antigen BCM1 precursor - mouse  
JL0143  
N:Alternate names: CD48 antigen homolog esp-60; OX45 antigen, Blast-1 antigen  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 31-Jan-2000  
C:Accession: JL0143; S21319; A47469  
R:Kong, Y.W.; Williams, A.F.; Kingmore, S.F.; Seidlin, M.F.  
J. Exp. Med. 171, 2115-2130, 1990  
A:Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1) region on mouse chromosome 3.  
A:Reference number: JL0143; MUID:90278362; PMID:1693656  
A:Accession: JL0143  
A:Molecule type: mRNA  
A:Residues: 1-240 <MON>  
A:Cross-references: EMBL:X17501; NID:950134; PIDN:CAA3542.1; PID:950135  
R:Kong, Y.W.; Williams, A.F.; Kingmore, S.F.; Seidlin, M.F.  
Submitted to the EMBL Data Library, June 1990  
A:Description: Structure, expression and genetic linkage of the mouse BCM1 (OX45 or Blast-1) region on mouse chromosome 3.  
A:Reference number: S21319  
A:Accession: S21319  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-240 <MON>  
A:Cross-references: EMBL:X5326; NID:950138; PIDN:CAA37604.1; PID:950139  
R:Cabreiro, J.G.; Freeman, G.J.; Lane, W.S.; Reiser, H.  
Proc. Natl. Acad. Sci. U.S.A. 90, 3418-3422, 1993  
A:Title: Identification, by protein sequencing and gene transfection, of esp-60 as the protein reference number: A47469; MUID:93234508; PMID:8475091  
A:Accession: A47469  
A:Molecule type: protein  
A:Residues: 74-80 <CAB>  
A:Experimental source: EL-4 lymphoma cells  
A:Note: sequence extracted from NCBI backbone (NCBI:P.129658)  
A:Accession: B47469  
A:Molecule type: protein  
A:Residues: 84-98 <CA2>  
A:Experimental source: EL-4 lymphoma cells  
A:Note: sequence extracted from NCBI backbone (NCBI:P.129660)  
C:Comment: This antigen is widely expressed on leukocytes and is likely to be anchored to the cell surface glycoprotein Blast-1  
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-217/Product: antigen BCM1 #status predicted <MAT>  
F:218-240/Domain: carboxyl-terminal propeptide #status predicted <CPT>  
F:22,38,70,136,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form)

Query Match 7.1%; Score 126.5; DB 2; Length 240;  
Best local similarity 21.4%; Pred. No. 0.0055;  
Matches 52; Conservative 45; Mismatches 125; Indels 21; Gaps 8;

QY 7 CLTLIYLMLQTLGSAASGPVKELVSGAVTFPL-KSKYKQVDSIVMTFNTPLVLTIP 65  
DB 9 CLVLELLLPGLGTFQGHSLIPDINATGTSNVLTKIHNDPLGPKRITLTKKQKILEV 68  
QY 66 EGGTIVTQNRNRRERDPDGGYSLSLTKSKKNDGSIYVIGIYSSLSQGSTQ-EVYLV 124  
DB 69 YNSTKTFSESEFGRAVYLENNALHISNRKDKGTYYRV---LRETNELKITLEV 124  
QY 125 YEHLSPKVTMGLOSKNGKCTVNTLTCMEHGSEEDVYTWKALGOANESHNGSIPISW 184  
DB 125 FQVPRPSEIINTKASTDSCHRLSC--EVKQHDYTYTSSGSPPKSPRYVDLV 182  
QY 185 RMGESDMTFICVARNPVSRN----FSSPI-LARK--LCEGAADDPSSNVLCLLVLP 236  
DB 183 TPONKSTFYCQVSNVSSKNDITVYFTLLPCDLARSSGVCWTA-----TWLVVTTLLIHR 237

QY 237 LUS 239  
DB 238 LUT 240

## RESULT 9

JH0395  
Biliary glycoprotein h precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 23-Jul-1999  
C:Accession: JH0395  
R:Kuraki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuo, Y.  
Biochem. Biophys. Res. Commun. 176, 578-585, 1991  
A:Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones for JH0395  
A:Reference number: JH0395; MUID:91222218; PMID:2025273  
A:Accession: JH0395  
A:Molecule type: mRNA  
A:Residues: 1-321 <KUR>  
A:Cross-references: GB:M69176; NID:G179434; PIDN:AAA51825.1; PID:G179435  
A:Experimental source: leukocyte  
C:Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.  
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal  
C:Keywords: glycoprotein; transmembrane protein  
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
F:139-321/Product: signal sequence #status predicted <SIG>  
F:160-217/Domain: immunoglobulin homology <IMM1>  
F:252-301/Domain: immunoglobulin homology <IMM2>

Query Match 7.1%; Score 125.5; DB 2; Length 321;  
Best local similarity 25.1%; Pred. No. 0.0094;  
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTITVQ-----NRRERVDPPDGGYSLSLTKSKKNDGSIYVIGIYSSLS-QQPSIOE 119  
DB 81 GYAIQTQATPSPANSRGRETI-YFNA--SLTLQNTQNTGTYTLQVIXSDLVNEBATQ 137  
QY 120 YVLHYEHLSPKRVMTMGLOSKNGKCTVNTLTCMEHGSEEDVYTWKALGOANESHNGSI 179  
DB 138 F-HVPELPKPSISISNNSNPVEDKDAVAFCT--EPTQDTYLLMT-----NNOS 184  
QY 180 LPISRW-----GESDMTFICVAR-----NPVSRFPSPILARKLCG-----A 218  
DB 185 LVSRLQLSNGNRITLTLSTVRNDTGPYECIQNPVSNRRDPV-TLVVYTGPDPTIS 243  
QY 219 ADD---PDSSNVLCLLI--VPLLSLFLVGLPLWFLKROEYIEKKKVDICRETP 272  
DB 244 PSDTYRPGANLSLSCYAASNPPAGYSWLINGTF-----QOSTQELPI-----P 287  
QY 273 NI-CPHSGENTRY--DTIHTRTILK 296  
DB 288 NITVNNSGSYTCHANNVYGCNRTYVK 314

## RESULT 10

JH0396  
Biliary glycoprotein i precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 23-Jul-1999  
C:Accession: JH0396  
R:Kuraki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuo, Y.  
Biochem. Biophys. Res. Commun. 176, 578-585, 1991  
A:Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones for JH0396  
A:Reference number: JH0396; MUID:91222218; PMID:2025273  
A:Accession: JH0396  
A:Molecule type: mRNA  
A:Residues: 1-351 <KUR>  
A:Cross-references: GB:M72238; NID:G179436; PIDN:AAA58393.1; PID:G179437  
A:Experimental source: leukocyte  
C:Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.  
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal  
C:Keywords: glycoprotein; transmembrane protein  
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F.1-34/Domain: signal sequence #status predicted <SIG>  
F.35-351/Product: biliary glycoprotein 1 #status predicted <MAT>  
F.160-217/Domain: immunoglobulin homology <IMM1>  
F.252-301/Domain: immunoglobulin homology <IMM2>

Query Match 7.1%; Score 125.5; DB 2; Length 351;  
Best Local Similarity 25.1%; Pred. No. 0.011;  
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

```
QY 68 GTITVTO-----NRNRVDFPDGYSGLSKLKNDSGIYVIGSSSL-QQPSIOE 119
DB 81 GYAIQTQATPGPAPNSGRRTI-YRNA--SLLIQNTQNDTGFTYLLQVIRSDLVNEBATQ 137
QY 120 YVLHYEHLSPKRVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQANESHNGSI 179
DB 138 F--HYPELPKPSISNNNSNPVEDKDAVAFTC--EPETQDTTYLMMI-----NNQS 184
QY 180 LPISRW-----GESDMTFICVAR-----NPVSRNFPSPILARKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRITLLSVTRNDTGPYCEIQNPVANSRSDPV-TLWVTYGPDPPTIS 243
QY 219 ADD----PDSMWVLLCLLL--VPLLSTFLVGLFLMFLRREGQEEYIEKKGVDCRETP 272
DB 244 PSDTYRRPANSLSLGYAASNPAPQYSWLINGTF-----QOSTQELFI-----P 287
QY 273 NI-CPHSGENTEX--DTIPHTNRITLK 296
DB 288 NITVNNSSGYTCHANNSTVGCNRTTYK 314
```

## RESULT 11

biliary glycoprotein g precursor - human  
JH0394  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 23-Jul-1999  
C:Accession: JH0394  
R:Kurcki, M.; Atakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuo, Y.  
Biochem. Biophys. Res. Commun. 176, 578-585, 1991  
A:Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr  
A:Reference number: JH0394; MUID:91222218; PMID:202573  
A:Accession: JH0394  
A:Molecule type: mRNA  
A:Residues: 1-417 <KUR>  
A:Cross-references: GB:M72238; NID:G179436; PIDN:AAA58394.1; PID:G179438  
A:Experimental source: leukocyte  
C:Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.  
C:Superfamily: carcinoembryonic antigen, carcinoembryonic antigen precursor amino-termi  
C:Keywords: glycoprotein, transmembrane protein  
F.1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
F.1-34/Domain: signal sequence #status predicted <SIG>  
F.35-383/Product: biliary glycoprotein g #status predicted <MAT>  
F.160-217/Domain: immunoglobulin homology <IMM1>  
F.252-301/Domain: immunoglobulin homology <IMM2>  
F.341-398/Domain: immunoglobulin homology <IMM3>

Query Match 7.1%; Score 125.5; DB 2; Length 417;  
Best Local Similarity 25.1%; Pred. No. 0.013;  
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

```
QY 68 GTITVTO-----NRNRVDFPDGYSGLSKLKNDSGIYVIGSSSL-QQPSIOE 119
DB 81 GYAIQTQATPGPAPNSGRRTI-YRNA--SLLIQNTQNDTGFTYLLQVIRSDLVNEBATQ 137
QY 120 YVLHYEHLSPKRVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQANESHNGSI 179
DB 138 F--HYPELPKPSISNNNSNPVEDKDAVAFTC--EPETQDTTYLMMI-----NNQS 184
QY 180 LPISRW-----GESDMTFICVAR-----NPVSRNFPSPILARKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRITLLSVTRNDTGPYCEIQNPVANSRSDPV-TLWVTYGPDPPTIS 243
QY 219 ADD----PDSMWVLLCLLL--VPLLSTFLVGLFLMFLRREGQEEYIEKKGVDCRETP 272
```

```
DB 244 PSDTYRRPANSLSLGYAASNPAPQYSWLINGTF-----QOSTQELFI-----P 287
QY 273 NI-CPHSGENTEX--DTIPHTNRITLK 296
DB 288 NITVNNSSGYTCHANNSTVGCNRTTYK 314
```

## RESULT 12:

transmembrane carcinoembryonic antigen 3 precursor - human  
C30127  
N:Alternate names: CD66 splice form BGPC  
C:Species: Homo sapiens (man)  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 23-Jul-1999  
C:Accession: C30127; 152597  
R:Barrett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K  
J. Cell Biol. 108, 267-276, 1989  
A:Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs  
A:Reference number: A52752; MUID:89139550; PMID:2537311  
A:Accession: C30127  
A:Molecule type: mRNA  
A:Residues: 1-464 <BAR>

A:Cross-references: EMBL:X16356; EMBL:X14784  
R:Mat, S.M.; Fawcett, J.; Murdoch, S.J.; Teixeira, A.M.; Geschmeissner, S.E.; Hajibagher  
Blood 84, 200-210, 1994  
A:Title: CD66 identifies the biliary glycoprotein (BGP) adhesion molecule: cloning, exp  
A:Reference number: 152597; MUID:94289702; PMID:8018919  
A:Accession: 152597  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-464 <RES>  
A:Cross-references: GB:S71326; NID:G550030; PIDN:AAB31183.1; PID:G550031  
C:Superfamily: carcinoembryonic antigen, carcinoembryonic antigen precursor amino-termi  
C:Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protei  
F.1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
F.1-34/Domain: signal sequence #status predicted <SIG>  
F.35-464/Product: transmembrane carcinoembryonic antigen 3 #status predicted <MAT>  
F.160-217/Domain: immunoglobulin homology <IMM1>  
F.252-301/Domain: immunoglobulin homology <IMM2>  
F.341-398/Domain: immunoglobulin homology <IMM3>  
F.424-455/Domain: transmembrane #status predicted <TM>  
F.104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405/Bindin

Query Match 7.1%; Score 125.5; DB 2; Length 464;  
Best Local Similarity 25.1%; Pred. No. 0.015;  
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

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QY 68 GTITVTO-----NRNRVDFPDGYSGLSKLKNDSGIYVIGSSSL-QQPSIOE 119
DB 81 GYAIQTQATPGPAPNSGRRTI-YRNA--SLLIQNTQNDTGFTYLLQVIRSDLVNEBATQ 137
QY 120 YVLHYEHLSPKRVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQANESHNGSI 179
DB 138 F--HYPELPKPSISNNNSNPVEDKDAVAFTC--EPETQDTTYLMMI-----NNQS 184
QY 180 LPISRW-----GESDMTFICVAR-----NPVSRNFPSPILARKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRITLLSVTRNDTGPYCEIQNPVANSRSDPV-TLWVTYGPDPPTIS 243
QY 219 ADD----PDSMWVLLCLLL--VPLLSTFLVGLFLMFLRREGQEEYIEKKGVDCRETP 272
DB 244 PSDTYRRPANSLSLGYAASNPAPQYSWLINGTF-----QOSTQELFI-----P 287
QY 273 NI-CPHSGENTEX--DTIPHTNRITLK 296
DB 288 NITVNNSSGYTCHANNSTVGCNRTTYK 314
```

## RESULT 13

biliary glycoprotein 1 precursor, splice form a - human  
A32164  
N:Alternate names: transmembrane carcinoembryonic antigen 1 (TM1-CEA); transmembrane car  
N:Contains: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice form x  
C:Species: Homo sapiens (man)

C>Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 20-Apr-2000  
 C/Accession: A32164; A30127; E0127; A48078; S45664; S65339; A30847; G44476  
 R/Hinda, Y.; Nematier, M.; Hefta, S.A.; Dizenfick, Z.; Wagener, C.; Shively, L.; Hefta, Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989  
 A/Reference number: A32164  
 A/Contents: extratum  
 A/Accession: A32164  
 A/Molecule type: mRNA  
 A/Residues: 1-526 <HIN>  
 A/Cross-references: GB:003858; NID:g179439; PIDN:AAA51826.1; PID:g179440  
 R/Hinda, Y.; Nematier, M.; Hefta, S.A.; Dizenfick, Z.; Wagener, C.; Shively, L.; Hefta, Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988  
 A/Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of  
 A/Reference number: A94206; MUID:88320555; PMID:2457922  
 A/Contents: annotation  
 A/Note: the sequence shown in this reference has been completely corrected in reference  
 R/Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K J. Cell Biol. 108, 267-276, 1989  
 A/Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNA  
 A/Reference number: A92752; MUID:89139550; PMID:257311  
 A/Accession: A30127  
 A/Molecule type: mRNA  
 A/Residues: 1-526 <BAR3>  
 A/Cross-references: EMBL:X16354; NID:g37197; PIDN:CAA34404.1; PID:g37198; EMBL:X14784  
 A/Experimental source: splice form a  
 A/Accession: B30127  
 A/Molecule type: mRNA  
 A/Residues: 1-319, 'P', 417-526 <BAR3>  
 A/Cross-references: EMBL:X14831; NID:g37199; PIDN:CAA32940.1; PID:g37200; EMBL:X14784  
 A/Experimental source: splice form b  
 R/Barnett, T.R.; Drake, L.; Pickle II, W. Mol. Cell. Biol. 13, 1273-1282, 1993  
 A/Title: Human biliary glycoprotein gene: characterization of a family of novel alternat  
 A/Reference number: A48078; MUID:93140765; PMID:8423792  
 A/Accession: A48078  
 A/Molecule type: mRNA  
 A/Residues: 124-141, 'H', 417-526 <BAR3>  
 A/Cross-references: GB:M76742; NID:g179480; PIDN:AAA57142.1; PID:g179481  
 A/Experimental source: splice form x  
 A/Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBI:123606)  
 R/Hauch, M.; Nedellec, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N. Eur. J. Biochem. 223, 529-541, 1994  
 A/Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene fami  
 A/Reference number: S45664; MUID:9433343; PMID:8055923  
 A/Accession: S45664  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-21 <HAN>  
 A/Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777  
 R/Nedellec, P.; Turbide, C.; Beauchemin, N. Eur. J. Biochem. 231, 104-114, 1995  
 A/Title: Characterization and transcriptional activity of the mouse biliary glycoprotein  
 A/Reference number: S65339; MUID:95354678; PMID:7628460  
 A/Accession: S65339  
 A/Status: preliminary  
 A/Molecule type: translation not shown  
 A/Residues: 1-21 <NRD>  
 A/Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992  
 R/Khan, W.N.; Friesenmyr, L.; Teglund, S.; Israelsson, A.; Bremner, K.; Hammarstrom, S. Genomics 14, 384-390, 1992  
 A/Title: Identification of three new genes and estimation of the size of the carcinoemb  
 A/Reference number: A44476; MUID:93052339; PMID:1427854  
 A/Contents: annotation; alignment of related sequences  
 C/Genetic:  
 A/Genes: GDB:BGP  
 A/Cross-references: GDB:127992; OMIM:109770  
 A/Map position: 19q13.2-19q13.2  
 C/Keywords: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin  
 F/1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F/1-34/Domain: signal sequence #status predicted <SIG>  
 F/35-526/Product: biliary glycoprotein 1, splice form a #status predicted <MATA>  
 F/35-428/Domain: extracellular #status predicted <EXT>  
 F/35-319, 'D', 417-526/Product: biliary glycoprotein 1, splice form b #status predicted <F/35-141, 'H', 417-526/Product: biliary glycoprotein 1, splice form x #status predicted <F/160-217/Domain: immunoglobulin homology <IMM1>  
 F/252-301/Domain: immunoglobulin homology <IMM2>  
 F/341-398/Domain: immunoglobulin homology <IMM3>  
 F/425-454/Domain: transmembrane #status predicted <TM>  
 F/453-526/Domain: intracellular #status predicted <INT>  
 F/104, 111, 115, 152, 182, 197, 208, 224, 232, 254, 274, 288, 292, 302, 309, 345, 351, 363, 378, 405, 475/B

Query Match 7.1%; Score 125.5; DB 1; Length 526;  
 Best Local Similarity 25.1%; Pred No. 0.017;  
 Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

Qy 68 GTITVQ-----NNRRVDFPDGYSKLKSKKNDGYYVYSSS- QQPSTGE 119  
 Db 81 GVALGTQATPPGANGRETI-YPNA-SLLIQNTQNDTGFTYLVKIDLVNEATGQ 137  
 Qy 120 YVLATYEHLSKPKVTMGLOSNNKGTCTVTLTCMEHGEEDVYITWKALQANESNGSI 179  
 Db 138 F-HVPELPKPSISSNNSNPVEDKDAVAFTC--BEETDITYLWMI-----NNQS 184  
 Qy 180 LPISRW-----GSDWTFICVAR-----NPVSNFSSPILARKLCEG-----A 218  
 Db 185 LPVSPRLQSLNGNRITLISVTRNDTGPCEIQLNPVSNRSDPV-TLAVYTGPTPTTS 243  
 Qy 219 ADD---PDSWVLLCLTL--VPLLSLPVLGLFLWFLKRRGEYIEBKRVDCRETP 272  
 Db 244 PSDTYRPGANSLSCYAASNPQAGSWLNGTF---QQSQELFI-----P 287  
 Qy 273 NI-CPSGENTEX--DTIHTNRITLK 296  
 Db 288 NITVNNSSGYTCHANNVSGCNRTTVK 314

RESULT 14  
 A27881  
 nonspecific cross-reacting antigen precursor - human  
 N/Alternate names: NCA; TEX/NCA  
 C/Species: Homo sapiens (man)  
 C/Date: 31-Mar-1989 #sequence revision 16-Sep-1992 #text change 31-Jan-2000  
 A/Accession: A26902; A29875; A27681; B31037; A29918; A27709; A26271; C26414; E44476; F4  
 R/Oikawa, S.; Kobaki, G.; Nakazato, H. Biochem. Biophys. Res. Commun. 146, 464-469, 1987  
 A/Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gen  
 A/Reference number: A26902; MUID:87298464; PMID:3619891  
 A/Accession: A26902  
 A/Molecule type: DNA  
 A/Residues: 1-141 <OIK>  
 A/Cross-references: GB:M17082; NID:g180230; PIDN:AAA51971.1; PID:g55322  
 R/Thompson, J.A.; Pandey, H.; Paxson, R.J.; Shively, L.; Padma, A.; Slimer, R.L.; Todd, P. Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987  
 A/Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fam  
 A/Reference number: A29875; MUID:87204248; PMID:3033672  
 A/Accession: A29875  
 A/Molecule type: DNA  
 A/Residues: 23-141 <THO>  
 A/Cross-references: GB:M16337  
 A/Note: the authors translated the codon ACT for residue 64 as Tyr  
 R/Tawarayagi, Y.; Oikawa, S.; Matsuo, Y.; Kobaki, G.; Nakazato, H. Biochem. Biophys. Res. Commun. 150, 89-96, 1988  
 A/Title: Primary structure of nonspecific crossreacting antigen (NCA), a member of carc  
 A/Reference number: A27681; MUID:88106638; PMID:333731  
 A/Accession: A27681  
 A/Molecule type: mRNA  
 A/Residues: 1-238, 'V', 240-344 <TAW>  
 A/Cross-references: GB:M18728; NID:g189084; PIDN:AAA59907.1; PID:g189085  
 R/Barnett, T.; Goebel, S.J.; Northcutt, M.A.; Elting, J.J. Genomics 3, 59-66, 1988  
 A/Title: Carcinoembryonic antigen family: characterization of cDNA coding for NCA and  
 A/Reference number: A31037; MUID:89122014; PMID:3220478

A:Accession: B31037  
 A:Molecule type: mRNA  
 A:Residues: 1-137, 'L', 139-344 <BAR>  
 A:Cross-references: GB:M2541; NID:G189103; PIDN:AA59915.1; PID:G189104  
 A:Note: the authors translated the codon TTG for residue 138 as Phe  
 R:Neumaier, M.; Zimmermann, W.; Shively, L.; Hnoda, Y.; Riggs, A.D.; Shively, J.E.  
 J. Biol. Chem. 263, 3202-3207, 1988  
 A:Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen (NC  
 A:Reference number: A29918; MUID:88139389; PMID:2830274  
 A:Accession: A29918  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <NEU>  
 A:Cross-references: GB:M18216; GB:J03550; NID:G178690; PIDN:AA51739.1; PID:G178691  
 R:Grumet, F.; Kolbinger, F.; Schwarz, K.; Schwalbold, H.; von Kleist, S.  
 Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988  
 A:Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and ind  
 A:Reference number: A27709; MUID:88268882; PMID:3390172  
 A:Accession: A27709  
 A:Molecule type: protein  
 A:Residues: 35-95; 99-120; 123-138; 149-151, 'X', 153-162; 166, 'X', 168-172, 'X', 174-193; 231-235  
 R:Hefla, S.A.; Paxton, R.J.; Shively, J.E.  
 J. Biol. Chem. 265, 8618-8626, 1990  
 A:Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci  
 A:Reference number: A36271; MUID:90256782; PMID:2341397  
 A:Accession: A36271  
 A:Molecule type: protein  
 A:Residues: 35-42; 44-53; 55-80; 83-134; 139-160; 166-172; 174-180; 191-194; 204-224; 233-308; 310  
 R:Paxton, R.J.; Mosser, G.; Pande, H.; Lee, T.D.; Shively, J.E.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987  
 A:Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation  
 A:Reference number: A26414; MUID:87147209; PMID:3469650  
 A:Accession: C26414  
 A:Molecule type: protein  
 A:Residues: 35-69 <PAX>  
 A:Status: preliminary; not compared with conceptual translation  
 A:Residues: 35-141 <KHA>  
 A:Accession: F44476  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 35-137, 'L', 139-141 <KH2>  
 C:Comment: This protein appears to be processed at the carboxyl terminus and anchored th  
 C:Genetics: GDB:NCA  
 A:Gene: GDB:NCA  
 A:Cross-references: GDB:120221; OMIM:163980  
 A:Map position: 19q13.2-19q13.2  
 A:introns: 22/1  
 A:Note: the list of introns may be incomplete  
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin  
 C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphat  
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
 F:1-134/Domain: signal sequence #status predicted <Sig>  
 F:35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>  
 F:160-217/Domain: immunoglobulin homology <IMM1>  
 F:252-301/Domain: immunoglobulin homology <IMM2>  
 F:321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
 F:104,111,115,127,137,197,224,256,274,288,292/Binding site: carbohydrate (Aen) (covalent  
 F:309/Binding site: carbohydrate (Aen) (covalent) #status predicted  
 F:320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

Query Match 7.0%; Score 124.5; DB 2; Length 344;  
 Best Local Similarity 22.4%; Pred. No. 0.012;  
 Matches 75; Conservative 35; Mismatches 118; Indels 107; Gaps 16;

QY 53 WTFTNTPLVLTIO-----PEGGTTI-----VTQNR-----NRERVD----- 82  
 DB 28 WSPPTTAKLTISTEPNVAEGKVELLALHNLPQNRIGISWYKGERVDGNSLIIVGYIGTQ 87

QY 83 -FPDGY-----SLKLSKLKNDSGIYVYSSSL-QQPSQOEYVLAVYEHL 129  
 DB 88 QATPGPAVSGRETIYVNSLLIQNTQNDTGFTYTLQVKSPLVNEATGQF--HYYPELP 145  
 QY 130 KKKVTMGISQNSKNGCTVNLTCMEHGEDVYTTKALGOANESHNSILPISRW--- 186  
 DB 146 KRSISSNNSNPVEDKDAVAFTC--EPEVQNTTYLMWV-----NQSLPVSPLQLS 194  
 QY 187 -GESDMTFI-----CYARPVRNFSPIIARLKC-----EGAADPPDS 225  
 DB 195 NQNMFTLLISVGRNDAGSECEIQNPASNSDPYTLNVLVGPDPPTISPSKANTPQEN 254  
 QY 226 WYLLCLLP--VPLLSLFLVLGLFLFKRQOEYIEKRVDCRETPNTI----- 274  
 DB 255 IMLSCHAAASNPAQSWFINGTF-----QQSQGELPI-----PNIVNNGSGYM 298  
 QY 275 CPHSQENTRYDTIPIPTNTILKEDPANTVYSVEI 309  
 DB 299 COAHNSATGLNRTVTMTVTSQSAFVLSAVAVTGI 333

## RESULT 15

S34338  
 Biliary glycoprotein F - mouse  
 N:Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein  
 C:Species: Mus musculus (house mouse)  
 C:Date: 23-Feb-1995 #sequence revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S34338; JCI510; K41093  
 R:Huang, J.C.; Huang, X.F.; Novel, M.; Novel, G.  
 submitted to the EMBL Data Library, July 1992  
 A:Description: A CIP-family gene present on the lactose-protease plasmid of lactococcus  
 A:Reference number: S34338  
 A:Accession: S34338  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-521 <HUA>  
 A:Cross-references: EMBL:X67281; NID:G312585; PIDN:CAA47696.1; PID:G312586  
 R:McCuig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.  
 Gene 127, 173-183, 1993  
 A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro  
 A:Reference number: JCI505; MUID:93273228; PMID:8500759  
 A:Accession: JCI510  
 A:Molecule type: mRNA  
 A:Residues: 1-81, 'Q', 83-141, 'P', 143-521 <MCC>  
 A:Cross-references: GB:X67281  
 R:Williams, R.K.; Jiang, G.S.; Holmes, K.V.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991  
 A:Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen  
 A:Reference number: A41093; MUID:91288498; PMID:1648219  
 A:Accession: A41093  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 35-59 <WIL>  
 C:Comment: This protein is expressed at the cell surface and plays a determinant role in  
 C:Genetics: GDB:BP  
 A:Gene: Bgpf  
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin  
 C:Keywords: glycoprotein; receptor  
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>  
 F:160-219/Domain: immunoglobulin homology <IMM1>  
 F:254-303/Domain: immunoglobulin homology <IMM2>  
 F:339-396/Domain: immunoglobulin homology <IMM3>  
 F:87,104,148,159,206,210,226,256,290,294,304,333,375/Binding site: carbohydrate (Aen) (c

Query Match 6.9%; Score 122.5; DB 2; Length 521;  
 Best Local Similarity 22.4%; Pred. No. 0.03;  
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QY 53 WTFTNTPLVLTIO-----PEGGTTIYQNR-----NRERVDPPDG-- 86  
 DB 28 WSPPTTAEVTEIENVPPQVAEDNNVLLVHNLPALGAPAKYKGNVSNABIVHEFTGTN 87  
 QY 87 -----GYSLKLSKLKNDSGIYVYSSSLQOPSTOEYV-LHYEHL 129

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Db      88 KTTGPAHSGRETVYSNGSLLIQRYTKDYGVTIEMTDENFR--TEATVQFHVHQLL 145
Qy     130 KPKVTWGLQSNKNGTCTNLTCCMEHGEEDVITYWKALGOANESHNGSILPISRWGES 189
Db     146 KPNITSNNSNPVSGDSDSVSLTCDSYTDPDNITYLMSRNGESLSE--GDRLKLS--EGNR 200
Qy     190 DMT-----FICVARNPVSRNFPSSP 208
Db     201 TLTLNVTNRNDTGPRVCETRNPVSVNRSDP 230

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Search completed: August 18, 2004, 16:09:01  
 Job time : 19 secs

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## OM protein - protein search, using SW model

Run on: August 18, 2004, 16:01:30 ; Search time 13 Seconds

(Without alignments)  
1341.808 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772  
Sequence: 1 MAGSPRTCLTYITLMQUTGS.....PHSLTMPDTPPLFAVENYI 335Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	354.5	20.0	654	1	LY9_MOUSE
2	318	17.9	655	1	LY9_HUMAN
3	186	10.5	343	1	SLAM_MOUSE
4	182.5	10.3	335	1	SLAM_HUMAN
5	144	8.1	344	1	CD2_MOUSE
6	134	7.6	240	1	CD48_MOUSE
7	133.5	7.5	351	1	CD2_HUMAN
8	130	7.3	344	1	CD2_RAT
9	126.5	7.1	240	1	CD48_MOUSE
10	125.5	7.1	526	1	CEA1_HUMAN
11	124.5	7.0	344	1	CEA8_HUMAN
12	119.5	6.7	365	1	CXAR_HUMAN
13	116.5	6.6	319	1	A33_HUMAN
14	114.5	6.5	702	1	CEA5_HUMAN
15	113.5	6.4	521	1	CEA1_MOUSE
16	110.5	6.2	463	1	CD4_CANFA
17	105.5	6.0	329	1	CD86_HUMAN
18	102.5	5.8	519	1	BCD2_RAT
19	101	5.7	349	1	CEA8_HUMAN
20	101	5.7	349	1	LACH_SCHAM
21	101	5.7	588	1	CL66_CHICK
22	100.5	5.7	555	1	CL66_CARAU
23	99	5.6	526	1	FVR_CERAE
24	98.5	5.6	417	1	BUTY_BOVIN
25	98	5.5	347	1	CD2_HORSE
26	98	5.5	503	1	SHS1_HUMAN
27	98	5.5	1382	1	MET_RAT
28	97	5.5	773	1	PIGR_RABIT
29	96	5.4	359	1	LACH_DROME
30	96	5.4	1087	1	BUTY_HUMAN
31	96	5.4	1451	1	PGDS_XENTIA
32	96	5.4	1451	1	MYM1_HUMAN
33	95.5	5.4	365	1	CXAR_MOUSE

34	95.5	5.4	700	1	PTPE_HUMAN
35	95.5	5.4	771	1	PIGR_MOUSE
36	95.5	5.4	822	1	CAN3_SHEEP
37	94	5.3	233	1	GP42_RAT
38	94	5.3	1088	1	NCA1_XENTIA
39	93	5.2	419	1	PGS4_HUMAN
40	93	5.2	419	1	PGS7_HUMAN
41	93	5.2	535	1	PYRG_SPICI
42	92.5	5.2	299	1	JAM1_HUMAN
43	92.5	5.2	330	1	CD86_RABIT
44	92.5	5.2	564	1	CL66_BRARE
45	91	5.1	491	1	KCS3_RABIT
46	91	5.1	822	1	CAN3_BOVIN
47	91	5.1	1548	1	SMCY_MOUSE
48	90.5	5.1	417	1	PVR_HUMAN
49	90.5	5.1	1905	1	Y659_PASWU
50	90	5.1	250	1	LFPA3_HUMAN
51	90	5.1	419	1	PSG1_HUMAN
52	90	5.1	541	1	IR18_HUMAN
53	89.5	5.1	243	1	CD48_HUMAN
54	89.5	5.1	349	1	OMPA_BUCAT
55	89.5	5.1	821	1	CAN3_PIG
56	89.5	5.1	1051	1	YC94_HUMAN
57	89	5.0	309	1	CD86_MOUSE
58	89	5.0	821	1	CAN3_HUMAN
59	88.5	5.0	327	1	OX2V_KSHV
60	88.5	5.0	1390	1	MOXR_RAT
61	88.5	5.0	363	1	MURG_BORBU
62	88	5.0	508	1	CD65_DROME
63	88	5.0	509	1	SHS1_RAT
64	88	5.0	530	1	PVR2_MOUSE
65	88	5.0	699	1	PTPE_MOUSE
66	88	5.0	821	1	CAN3_RAT
67	88	5.0	1092	1	NCA2_XENTIA
68	88	5.0	6669	1	NEBU_HUMAN
69	87.5	4.9	265	1	CEAT_HUMAN
70	87.5	4.9	422	1	KI11_RAT
71	87.5	4.9	769	1	PIGR_RAT
72	87.5	4.9	457	1	CD4_MOUSE
73	87	4.9	491	1	KCS3_HUMAN
74	87	4.9	583	1	CL66_HUMAN
75	87	4.9	1666	1	MYM1_MOUSE
76	87	4.9	3707	1	PGM1_MOUSE
77	87	4.9	443	1	EXTL_VJBVU
78	86.5	4.9	348	1	KI10_RAT
79	86	4.9	354	1	VGL1_VZVD
80	86	4.8	978	1	KFMS_FSVMD
81	85.5	4.8	2491	1	MPRI_HUMAN
82	85.5	4.8	402	1	RAGE_RAT
83	85	4.8	428	1	PSG3_HUMAN
84	85	4.8	821	1	CAN3_MOUSE
85	84.5	4.8	292	1	Y152_HUMAN
86	84.5	4.8	583	1	CL66_MOUSE
87	84.5	4.8	1211	1	MI01_HUMAN
88	84.5	4.8	668	1	PBS7_VRAST
89	84	4.7	1300	1	IRR_MOUSE
90	84	4.7	1379	1	MET_MOUSE
91	84	4.7	3034	1	CLRI_MOUSE
92	84	4.7	298	1	JAM2_HUMAN
93	83.5	4.7	463	1	STHA_PSEFL
94	83	4.7	757	1	PIGR_BOVIN
95	83	4.7	873	1	LDVA_HUMAN
96	83	4.7	1106	1	ACTV_CAEEL
97	83	4.7	773	1	MES2_CAEEL
98	82.5	4.7	386	1	NATB_BACSU
99	82	4.6	609	1	HEMA_RINDR
100	82	4.6	880	1	TYO3_MOUSE
101	82	4.6	1007	1	GRD2_HUMAN
102	82	4.6	102	1	PGCV_CHICK
103	82	4.6	3562	1	OX26_RAT
104	81.5	4.6	302	1	ICOL_HUMAN
105	81.5	4.6	378	1	LEUK_RAT
106	81.5	4.6			

P23469	homo sapien
O70570	mus musculus
O9c7b8	ovis aries
P23505	rattus norv
P16170	xenopus lae
O00868	homo sapien
O13046	homo sapien
P52200	spiloplasma
O9y624	homo sapien
P42071	oryctolagus
O94040	brachydontio
O9ct17	oryctolagus
P51186	bos taurus
O62240	mus musculus
P15151	homo sapien
O9cm21	pasteurella
P19256	homo sapien
P11464	homo sapien
O13478	homo sapien
P09326	homo sapien
P57414	buchnera ap
P43368	bos taurus
O9p2q2	homo sapien
P42082	mus musculus
P20807	homo sapien
P88963	kaposi's sa
O9e588	rattus norv
P08581	homo sapien
O51708	borrelia bu
O9vfp1	drosoophila
P97710	l protein-t
P32507	mus musculus
P49446	mus musculus
P16259	rattus norv
P36335	xenopus lae
P20929	homo sapien
O14002	homo sapien
P83556	rattus norv
P15083	rattus norv
P06332	mus musculus
O9bq41	homo sapien
O13740	homo sapien
O62234	mus musculus
O05793	mus musculus
O8df55	vibrio vuln
O9z018	rattus norv
P09258	varicella-z
P11717	homo sapien
P00545	feline sarc
O16549	rattus norv
O16557	homo sapien
O64651	mus musculus
O14165	homo sapien
O61490	mus musculus
O9bxc6	homo sapien
P08018	saccharomyc
O9wt14	mus musculus
P16056	mus musculus
O35161	mus musculus
P57087	homo sapien
O05139	pseudomonas
P81265	bos taurus
P98155	homo sapien
P53855	caenorhabdi
O15154	caenorhabdi
P46954	caecilius su
P41555	rinderpest
P55144	mus musculus
O43424	homo sapien
O90553	gallus gall
P04212	rattus norv
O75144	homo sapien
P13838	rattus norv











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691 67 3.8 320 1 RLUB_VIBVU Q8d8c0 vibrio vuln
692 67 3.8 358 1 BIOB_METJA Q58692 methanococ
693 67 3.8 371 1 CRU2_HUMAN Q9h673 homo sapien
694 67 3.8 373 1 REPT_YRST P03871 saccharomyc
695 67 3.8 401 1 ASST_STRAP Q8c9u3 staphylococ
696 67 3.8 413 1 HEMO_MANSE P31992 manduca sex
697 67 3.8 495 1 CD5_HUMAN P06127 homo sapien
698 67 3.8 501 1 CPUS_MOUSE O54749 mus musculu
699 67 3.8 524 1 Y395_MYCGE P47635 mycoplasma
700 67 3.8 542 1 IMA1_SCHPO O14063 schizosacch

ALIGNMENTS

RESULT 1
LY9_MOUSE
ID LY9_MOUSE STANDARD; PRT; 654 AA.
AC Q01965; Q9ES29; Q9ES35; Q9ES36;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen 9)
DE (Cell-surface molecule Ly-9).
GN LY9 OR LY-9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A., AND POLYMORPHISM.
RC STRAIN=129/Sv, BALB/c, and C57BL/6; TISSUE=Spleen;
RX MEDLINE=20424510; PubMed=10970093;
RA Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
RT "Gene structure of the mouse leukocyte cell surface molecule Ly9.";
RT Immunogenetics 51:788-793(2000).
RN [2]
RN SEQUENCE OF 22-654 FROM N.A., AND SEQUENCE OF 48-59.
RX MEDLINE=92373005; PubMed=1506686;
RA Sandrin M.S., Gumley T.P., Henning M.M., Vaughan H.A., Genez L.J.,
RA Trapant J.A., McKenzie I.F.C.;
RT "Isolation and characterization of cDNA clones for mouse Ly-9.";
RT J. Immunol. 149:1636-1641(1992).
RL J. FUNCTION: May participate in adhesion reactions between T
CC lymphocytes and accessory cells by homophilic interaction.
CC SUBCELLULAR LOCATION: Type I membrane protein.
CC TISSUE SPECIFICITY: LYMPHOCYTES.
CC SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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CC -----
DR EMBL; AF244131; AAG14997.1; -
DR EMBL; AF244130; AAG14996.1; -
DR EMBL; AF246701; AAG13268.2; -
DR EMBL; AF245117; AAG13268.2; JOINED.
DR EMBL; AF24506; AAG13268.2; JOINED.
DR EMBL; AF245118; AAG13268.2; JOINED.
DR EMBL; AF24507; AAG13268.2; JOINED.
DR EMBL; AF24508; AAG13268.2; JOINED.
DR EMBL; AF24509; AAG13268.2; JOINED.
DR EMBL; AF24510; AAG13268.2; JOINED.
DR EMBL; AF246699; AAG13268.2; JOINED.
DR EMBL; AF246700; AAG13268.2; JOINED.
DR EMBL; M84412; AAA39468.1; -
DR HSPF; P08921; IHNG.
DR MGD; MGI:96885; LY9.
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DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
KW Cell adhesion; Antigen; Signal; Transmembrane; Glycoprotein;
KW Immunoglobulin domain; Repeat; Polymorphism.
FT SIGNAL 1 47
FT CHAIN 48 654
FT DOMAIN 48 453
FT TRANSMEM 454 474
FT DOMAIN 475 654
FT DOMAIN 48 158
FT DOMAIN 159 243
FT DOMAIN 250 362
FT DOMAIN 353 453
FT DISULFID 172 242
FT DISULFID 178 222
FT DISULFID 376 445
FT DISULFID 382 426
FT CARBOHYD 68 68
FT CARBOHYD 120 120
FT CARBOHYD 231 231
FT CARBOHYD 284 284
FT CARBOHYD 390 390
FT CARBOHYD 412 412
FT CARBOHYD 423 423
FT CARBOHYD 434 434
FT VARIANT 10 10
FT VARIANT 14 14
FT VARIANT 79 79
FT VARIANT 91 91
FT VARIANT 130 130
FT VARIANT 139 139
FT VARIANT 352 362
FT VARIANT 366 366
FT VARIANT 377 377
FT VARIANT 550 550
FT VARIANT 592 592
FT CONFLICT 283 283
FT CONFLICT 489 499
FT CONFLICT 560 560
FT CONFLICT 647 654
SQ SEQUENCE 654 AA; 73142 MW; 1CBBE9708A8EBE7 CRC64;

Query Match
Beet Local Similarity 27.6%; Pred. No. 6,8e-22;
Matches 118; Conservative 52; Mismatches 138; Indels 119; Gaps 16;

QY 14 LMQL-TGSA-----ASGPYKEIVGSGAVTEPLKSK-VKQYDSIVTENTPTPLVTIQPEG 67
DB 238 IWQFTGASRRKRTAAG--KITVGLIGEPVTLPLEFRARTRARKNVAVVENTS--VISQRR 293
QY 68 GTTIYVQNR---NREVPDPDGGYSLKSLKKNDGCIYVGYSSLOQPSQOEYVL 122
DB 294 GAATADSRKKPKSGSERRVRTSDQOSIKIKEDAPHAAYCSBASRDPVRRFTL 353
QY 123 HYVHELSKPKXTMGIGSKNGKTCVTNLCCMEHGEDVITYMKALGOANSHNGSTLPI 182
DB 354 LVYKRLKRPVTKSPVHMNGICEVVLTCVSVDGGNNVTYTMPLOKNAVNSQCKSHLV 413
QY 183 SWRMGSDMTFICVARNPVSRNPSPIILARKICEGADDDPSMWLCLILVPLLLSLFV 242
DB 414 SWESEGHLPNTFTCLAHNPVS--NSSQPSFGITCSG---PBRNRKRFWLLLLLVLLML 468
QY 243 LGLFLMFLKRE-----ROEYIEE-----KRVYDICTREFNIPC- 276
DB 469 GGYFTLRKKKCCSLATRYROAEVPAEIPETPTGHGQSVLSQRYEKLDMSAKTRHQP 528
QY 377 -----HSGENTE-----YDIIPTN----- 291
DB 529 PTDSTSSSSATTEBDEKTRMHSSTANSRNOYDVLVTHQDIAHALAYGQVEYEAITPYD 588
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QY 292 -----RTIL--KEDPANTVSTVEIPKK-MENPHSLLTWPDTP 326  
DB 589 KUDGSMDDEDMAYIOVSLNQGSTPLPQKEDSDNTTICSQVKPKKATQTPQDAESPETP 648  
QY 327 RLPAYEN 333  
DB 649 ---TYEN 652

RESULT 2  
LY9 HUMAN STANDARD; PRT; 655 AA.  
AC O9HBG7; Q14775; Q9H4N5; Q9NQ24;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE T-lymphocyte surface antigen Ly-9 precursor (lymphocyte antigen 9) (cell-surface molecule Ly-9) (CD229 antigen).  
GN LY9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI Taxid=9606;  
OX [1] \_SEQUENCE FROM N.A. (ISOFORM 1).  
RP MEDLINE=20424510; PubMed=1097093;  
RX Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;  
RT "Gene structure of the mouse leukocyte cell surface molecule Ly9.";  
RL Immunogenetics 51:788-793(2000).  
RN [2]  
RP SEQUENCE OF 32-654 FROM N.A. (ISOFORM 2).  
RX MEDLINE=96128248; PubMed=8537117;  
RA Sandlin M.S., Henning M.W., Lo M.F., Baker E., Sutherland G.R.,  
RT "Isolation and characterization of cDNA clones for HumLy9: the human homologue of mouse Ly9.";  
RL Immunogenetics 43:13-19(1996).  
RN [3]  
RP SEQUENCE OF 1-151 FROM N.A.  
RA Bates K.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 99-655 FROM N.A. (ISOFORM 3).  
RA Zhou J., Yu W., Tang H., Mei G., Tseng Y.T.M., Bouck J., Gibbs R.A.,  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: May participate in adhesion reactions between T lymphocytes and accessory cells by homophilic interaction.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Experimental confirmation may be lacking for some isoforms;  
CC Name=1;  
CC IsoId=Q9HBG7-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9HBG7-2; Sequence=VSP\_002525;  
CC Name=3;  
CC IsoId=Q9HBG7-3; Sequence=VSP\_002524, VSP\_002525, VSP\_002526;  
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.  
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CC  
CC EMBL; AF244129; AAC14995.1; -  
CC EMBL; LA2621; AAA92623.1; -  
CC EMBL; AL121985; CAC00580.1; -

DR EMBL; AY007142; AAC02002.1; -  
DR Genew; HGNC:6730; LY9.  
DR MIM; 600684; -  
DR GO; GO:0005887; C:integral to plasma membrane; ISS.  
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00409; Ig\_2.  
DR PROSITE; PS50835; Ig\_LIKE; 2.  
DR Cell adhesion; Antigen; Signal; Transmembrane; Glycoprotein;  
KW Immunoglobulin domain; Repeat; Alternative splicing.  
FT SIGNAL 1 47  
FT CHAIN 48 655  
FT DOMAIN 48 454  
FT TRANSMEM 455 476  
FT DOMAIN 477 655  
FT DOMAIN 48 158  
FT DOMAIN 159 235  
FT DOMAIN 251 363  
FT DOMAIN 364 452  
FT DISULFID 172 242  
FT DISULFID 178 222  
FT DISULFID 377 446  
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FT CARBOHYD 68 68  
FT CARBOHYD 95 95  
FT CARBOHYD 120 120  
FT CARBOHYD 169 169  
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FT CARBOHYD 285 285  
FT CARBOHYD 413 413  
FT CARBOHYD 424 424  
FT VARSPLIC 359 448  
FT VARSPLIC 500 513  
FT VARSPLIC 524 554  
FT CONFLICT 171 171  
FT CONFLICT 602 602  
SQ SEQUENCE 655 AA; 72107 MW; 9F80A3056D79F80A CRC64;  
Query Match 17.9%; Score 318; DB 1; Length 655;  
Best Local Similarity 30.3%; Pred. No. 7.6e-19;  
Matches 91; Conservative 49; Mismatches 128; Indels 32; Gaps 10;  
QY 19 GSASGPVKE-LVGSVGAVTPEPK-SVKQVDSIVTFNTPTPLVTOPEGGT---IIVT 73  
DB 246 GASRGSTTGTGVVGLGEPVTLPLALPACRDTKRWMLNFTLSISKREBAATADPLIKS 305  
QY 74 QNRNRERVPDPGVSLKLKLNKDSGIYVGIYSSLSQOSTOEVYLVHYEHLSPKV 133  
DB 306 RDPYKRWVWVSQDLSKLKIEDAGPYHAYVGEASVSMTHVTLLIYRLKPKI 365  
QY 134 TNGLSNKNKGTCTNLTCCMEHGEEDVYITWALGQANESHNGSLPLISMRKGEEDMTF 193  
DB 366 TWSLRSHSGICISITLTCVDEGQNTVMYTPLOKEAVVQGESHLNVSRSSEHNPML 425  
QY 194 ICVARNPVRNPSPIKLKCEGADDDSSVLLCLLVPLLSLFLVGLWFLKRE 253  
DB 426 TCTASNPVRS-SHOPLSENICSG---PERYKLMIGLF-LMVCLLCVGIFSKIC--- 475  
QY 254 ROBEYIEKKKRVDCIETFNICPHSGE---NTEYDTIPTNRTILKEDPANTVYSTVEIP 310  
DB 476 -----WKRGKRC-SVPAFCSQGEADADPPEPAFGHTLVSVLSQG-----YKLDTP 521

RESULT 3  
SLAM MOUSE STANDARD; PRT; 343 AA.  
AC Q9QUM4; Q9QX23;

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Signaling lymphocytic activation molecule precursor.  
 GN SLAMF1 OR SLAM.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).  
 RC STRAIN=BALB/c;  
 RX MEDLINE=20040375; PubMed=10570270;  
 RA Caserio A.G., Hauser T.M., Cocks B.G., Abrams J., Zurawski S.,  
 RA Chaturkova T., Zouin F., Robinson D., Tangye S.G., Averaa G.,  
 RA Nichols K.E., de Vries J.E., Lanier L.L., O'Garra A.;  
 RT "Molecular and functional characterization of mouse signaling  
 RT lymphocytic activation molecule (SLAM): differential expression and  
 RT responsiveness in Th1 and Th2 cells.";  
 RL J. Immunol. 163:5860-5870(1999).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG).  
 RA Wang N., Wu C., Sayos J., Terhorst C.;  
 RT "Genomic organization of murine SLAM";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: HIGH-AFFINITY SELF-LIGAND CONSIDERED TO BE IMPORTANT IN  
 CC BIRECTIONAL T <-> B-CELL STIMULATION. SLAM-INDUCED SIGNAL-  
 CC TRANSDUCTION EVENTS IN T LYMPHOCYTES ARE DIFFERENT FROM THOSE IN B  
 CC CELLS. TWO MODES OF SLAM SIGNALING ARE LIKELY TO EXIST: ONE IN  
 CC WHICH THE INHIBITOR SH2D1 ACTS AS A NEGATIVE REGULATOR AND  
 CC ANOTHER IN WHICH PROTEIN-TYROSINE PHOSPHATASE 2C (PTPN11)-  
 CC DEPENDENT SIGNAL TRANSDUCTION OPERATES.  
 CC -1- SUBUNIT: ITS CYTOPLASMIC DOMAIN INTERACTS WITH SH2 DOMAIN PROTEIN  
 CC 1A (SH2D1) THROUGH PART OF ITS SH2 DOMAIN, AND UPON TYROSINE  
 CC PHOSPHORYLATION WITH PTPN11, BUT NOT WITH SHP-1.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein; present on the  
 CC surface of B and T cells.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Long;  
 CC IsoId=Q9QUM4-1; Sequence=Displayed;  
 CC Name=Short;  
 CC IsoId=Q9QUM4-2; Sequence=VSP\_002570;  
 CC -1- PTM: Phosphorylated.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
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 CC -----  
 CC EMBL AF149791; AAF22231.1; -;  
 DR EMBL AF149792; AAF22232.1; -;  
 DR EMBL AF164523; AAF13818.1; -;  
 DR EMBL AF164519; AAF13818.1; JOINED.  
 DR EMBL AF164520; AAF13818.1; JOINED.  
 DR EMBL AF164521; AAF13818.1; JOINED.  
 DR EMBL AF164522; AAF13818.1; JOINED.  
 DR EMBL AF160990; AAF14535.1; -;  
 DR MGD; MGI:1351314; Slam.  
 DR InterPro: IPR007110; Ig-like.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Receptor; Signal; Transmembrane; T-cell; Glycoprotein; Repeat;  
 KW Immunoglobulin domain; Phosphorylation; Alternative splicing.  
 FT SIGNAL 1 24  
 FT CHAIN 25 343  
 FT DOMAIN 25 265  
 FT TRANSMEM 243 265  
 FT POTENTIAL.  
 FT MOLECULE.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.

FT DOMAIN 266 343 CYTOPLASMIC (POTENTIAL).  
 FT DOMIN 7 153 IG-LIKE V-TYPE.  
 FT DOMIN 145 228 IG-LIKE C2-TYPE.  
 FT DISULFD 161 232 BY SIMILARITY.  
 FT DISULFD 167 212 BY SIMILARITY.  
 FT SITE 286 291 SH2-BINDING (POTENTIAL).  
 FT SITE 313 318 SH2-BINDING (POTENTIAL).  
 FT SITE 333 338 SH2-BINDING (POTENTIAL).  
 FT CAREOHD 54 58 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CAREOHD 58 54 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CAREOHD 103 103 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CAREOHD 126 126 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CAREOHD 151 151 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CAREOHD 158 158 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CAREOHD 192 192 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CAREOHD 211 211 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CAREOHD 226 226 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT VARSPLC 236 343 POEKLHDALTDQDCCTTYVAATEPAPESVQEPPTVYA  
 FT SVTLPEP -> VRSMPLAGSVIFRTGFLAALHTTWLQ  
 FT GILE (in isoform short).  
 FT /FTId=VSP\_002570.  
 SQ SEQUENCE 343 AA; 38094 MW; 7980470157EB814C4 CRC64;  
 Query Match 10.5%; Score 186; DB 1; Length 343;  
 Best Local Similarity 24.3%; Pred. No. 3.7e-08;  
 Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;  
 QY 8 LTLIIIMQUNGSASG---PYKELVSGVGATFPL-----SKRVQYDSIVTFN 56  
 DB 12 LFLSLAELSLGTGGVMDCEV--TLQKLDQDTWLPTEHQINKSVNKSRIIVL-TWA 68  
 QY 57 TTPPLVITIOPEGTIIIVTONRRRERYDF-----PD-----SKLSKLKIND 99  
 DB 69 TSP-----GSKSNKKIYSPFLDSKSGYDHLDEGHHFQSKNLSKLKGNRES 115  
 QY 100 SGIIYVGIYSS-SLQGPSTQEVLVHVEHLSKP--KVTWGLQSNKNGTCVTNLTCCMEHG 156  
 DB 116 EGMVLYSVVENVSVQPCFKQ--LKLVEGVSPPEIKVINKTQENENGCTSLILACTVKGK 172  
 QY 157 EEDVITYMK-----ALGOANESHNGSLTPISWRGSDMFFICARVPV---SRNFSPP 208  
 DB 173 DH-VTYSWSDENGTHLSRNRSH--LHLTTLNQHODSYNTCTASNPVSSISRTFN-- 226  
 QY 209 ILARKLCRGAADDPSSMWLLCLLVPLLSLVGLFLMFLKRRQREYLE---EKXRV 265  
 DB 227 -LSGACQAGSSSSSPMMQYTIIVPLGVIIIFLVFTALIMMKRQSKNHQPPVBEKSL 285  
 QY 266 DICRETENICPHSGENTYDTIIPHTNRITLKBDPANTVY--SYVEIPKMEHP-----HS 318  
 DB 286 TIYAGVQKSGFO--EKKLHD-----ALTDODPCTTIYVAATEPAPESVQEPPTVYA 336  
 QY 319 LITMPTD 325  
 DB 337 SVTLPEP 343  
 RESULT 4  
 SLAM\_HUMAN STANDARD; PRT; 335 AA.  
 ID SLAM\_HUMAN  
 AC Q13291;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Signaling lymphocytic activation molecule precursor (IPO-3) (CD150  
 GN SLAMF1 OR SLAM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RC TISSUE=T-cell;

RX MEDLINE=95342241; PubMed=7617038;  
 RA Cocke B.G., Chang C.-C.J., Carballido J.M., Yssel H., de Vries J.E.,  
 RT "A novel receptor involved in T-cell activation.";  
 RL Nature 376:260-263(1995).  
 CC -1- FUNCTION: HIGH-AFFINITY SELF-LIGAND CONSIDERED TO BE IMPORTANT IN  
 BIDIRECTIONAL T <-> B-CELL STIMULATION. SLAM-INDUCED SIGNAL-  
 TRANSDUCTION EVENTS IN T LYMPHOCYTES ARE DIFFERENT FROM THOSE IN B  
 CELLS. TWO MODES OF SLAM SIGNALING ARE LIKELY TO EXIST: ONE IN  
 WHICH THE INHIBITOR SH2D1A ACTS AS A NEGATIVE REGULATOR AND  
 ANOTHER IN WHICH PROTEIN-TYROSINE PHOSPHATASE 2C (PTPN11) -  
 DEPENDENT SIGNAL TRANSDUCTION OPERATES.  
 CC -1- SUBUNIT: ITS CYTOPLASMIC DOMAIN INTERACTS WITH SH2 DOMAIN PROTEIN  
 1A (SH2D1A) THROUGH PART OF ITS SH2 DOMAIN, AND WITH PTPN11.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein; present on the  
 surface of B and T cells.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1; Synonyms=Long;  
 CC IsoId=Q13291-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Short;  
 CC IsoId=Q13291-2; Sequence=VSP\_002568, VSP\_002569;  
 CC Name=3; Synonyms=Secreted;  
 CC IsoId=Q13291-3; Sequence=VSP\_002567;  
 CC -1- TISSUE SPECIFICITY: Constitutively expressed on peripheral blood  
 memory T cells, T-cell clones, immature thymocytes, and a  
 proportion of B-cells, and is rapidly induced on naive T cells  
 after activation.  
 CC -1- DOMAIN: SH2 DOMAINS USE TO BIND TO PHOSPHOTYROSINE RESIDUES IN A  
 SEQUENCE-SPECIFIC MANNER. IN THIS CASE, HOWEVER, THE SPECIFIC  
 SH2D1A-BINDING SITE IS AROUND THE MOST MEMBRANE-PROXIMAL TYROSINE  
 RESIDUE (TYR-281) OF THE CYTOPLASMIC TAIL, AND PHOSPHORYLATION OF  
 TYR-281 IS NOT REQUIRED FOR BINDING.  
 CC -1- PTM: PHOSPHORYLATED BY FYN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide Cdw150 entry;  
 CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cdw150.htm".  
 CC -----  
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 or send an email to license@1sb-sib.ch).  
 CC -----  
 CC EMBL: U33017; AAA5380.1; -.  
 DR PIR: S58892; S58892.  
 DR PDB: 1D4T; 10-APR-00.  
 DR PDB: 1D4W; 04-APR-00.  
 DR PDB: 1KA6; 28-AUG-02.  
 DR PDB: 1KA7; 28-AUG-02.  
 DR Genew: HGNC:10903; SLAMF1.  
 DR MIM: 603492; -.  
 DR GO: GO:0003823; P:antigen binding; TAS.  
 DR GO: GO:0004888; P:transmembrane receptor activity; TAS.  
 DR GO: GO:0006560; P:antimicrobial humoral response (sensu Inver. . .); TAS.  
 DR GO: GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR InterPro: IPR007110; IG-like.  
 DR PROSITE: PS50835; IG-LIKE\_1.  
 KM Receptor; Signal; Transmembrane; T-cell; Antigen; Glycoprotein;  
 KM Repeat; Immunoglobulin domain; Phosphorylation; Alternative splicing;  
 KM 3D-structure.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 335 SIGNALING LYMPHOCYTIC ACTIVATION  
 FT MOLECULE.  
 FT DOMAIN 21 237 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 238 258 POTENTIAL.  
 FT DOMAIN 259 335 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 7 152 IG-LIKE V-TYPE.  
 FT DOMAIN 144 223 IG-LIKE C2-TYPE.  
 FT DISULFID 158 228 BY SIMILARITY.

FT DISULFID 164 209 BY SIMILARITY.  
 FT SITE 281 286 SH2-BINDING (POTENTIAL).  
 FT SITE 307 312 SH2-BINDING (POTENTIAL).  
 FT SITE 327 332 SH2-BINDING (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 234 263 Missing (in isoform 3).  
 FT VARSPLIC 289 298 /FTId=VSP\_002567.  
 FT VARSPLIC 299 335 /FTId=VSP\_002568.  
 FT VARSPLIC 335 Missing (in isoform 2).  
 FT VARSPLIC 335 /FTId=VSP\_002569.  
 SQ SEQUENCE 335 AA; 37231 MW; BFB0F27EA31D8C04 CRC64;  
 Query Match 10.3%; Score 182.5; DB 1; Length 335;  
 Best Local Similarity 22.5%; Pred. No. 7e-08;  
 Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;  
 QY 8 LRLIYILW-QLTGSASGP-----VKELVSGVGAATPPL-----KSKVKQVDSIVWT 54  
 DB 7 LSLTFVLFSLAFGASVGTGRMNCPKILRQSGVLLPLTYERINKSMNSIHIVTM 66  
 QY 55 FMT-----TPVLTTP-EGTIIYVQNRRRDEPDGYSIKLSKLNKDGIIYVGI 107  
 DB 67 AKSLNSVENKIYSLDPSESG-----PPRYLGRKYRYLENTLIGHSRKEDEGWYLTML 122  
 QY 108 YSS-SLQDSTQRYVLAHYEHSKPYTWGLQSNKRGTCYTNLTCCMEHGEEDVIYTW-- 164  
 DB 123 EKRVSVQRCLQ---LRLVEQVSTPEIKVINKTEGNETTLIGCTYVEKGDH-VAVSWSE 178  
 QY 165 KALQGANSHSGSILPIRMWGESDMTFICVARNVSRNFS--SPILARKLCEGAADP 222  
 DB 179 KAGTHPLNPNANSHLSLTGPOHADNITYICTVSNPISNSQFSP-----WPGCRTP 232  
 QY 223 DSGM-----VLCILVPLLSFVLGLFPLPKRQREYIE--EKKRVDIC 268  
 DB 233 SERKPAAVYAGLLGIVIMILINVLQ-----LRRGKTHYQTYVEKSLITY 281  
 QY 269 RETPNICPSGSGENTEDTPTNRTIKLKDPAITY--STVEPKMKNPHSL-----LT 331  
 DB 282 AQVQKQGP---LQKKIDSPF-----ADPCTTIYVAATPEVPSVOETNSITYVASYT 331  
 QY 322 MPDT 325  
 DB 332 LPES 335  
 RESULT 5  
 ID\_CD2\_MOUSE STANDARD; PRT; 344 AA.  
 AC P08920; Q61394;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE T-cell surface antigen CD2 precursor (T-cell surface antigen  
 DE T11/Leu-5) (LFA-2) (LFA-3 receptor).  
 GN CD2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B10.A;  
 RC MEDLINE=87276135; PubMed=2440689;  
 RA Sewell W.A., Brown M.H., Fink P.J., Kozak C.A., Crumpton M.J.;  
 "The murine homologue of the T lymphocyte CD2 antigen: molecular

RT cloning, chromosome assignment and cell surface expression.";  
 RL Eur. J. Immunol. 17:1015-1020(1987).  
 (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86004738; PubMed=2820751;  
 RA Clayton L.K., Sayre P.H., Novotny J., Reinherz E.L.;  
 RT "Murine and human T11 (CD2) cDNA sequences suggest a common signal  
 transduction mechanism.";  
 RL Eur. J. Immunol. 17:1367-1370(1987).  
 (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Liver;  
 RX MEDLINE=88140313; PubMed=2894031;  
 RA Diamond D.J., Clayton L.K., Sayre P.H., Reinherz E.L.;  
 RT "Exon-intron organization and sequence comparison of human and murine  
 T11 (CD2) genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1615-1619(1988).  
 (4)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88140313; PubMed=3257775;  
 RA Yagita H., Okumura K., Nakauchi H.;  
 RT "Molecular cloning of the murine homologue of CD2. Homology of the  
 molecule to its human counterpart T11.";  
 RL J. Immunol. 140:1321-1326(1988).  
 (5)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Hematopoietic;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 Brownstein M.J., Usdn T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 Bosak S.A., Mesman P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 Scherch A., Schein J.E., Jones S.J.M., Marz M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 (6)  
 RP INTERACTION WITH CD2AP.  
 RX MEDLINE=98412662; PubMed=9741631;  
 RA Dustin M.L., Oleszowy M.W., Holdorf A.D., Li J., Bromley S., Desai N.,  
 Wilder P., Rosenberger F., van der Merwe P.A., Allen P.M., Shaw A.S.;  
 RT "A novel adaptor protein orchestrates receptor patterning and  
 cytoskeletal polarity in T-cell contacts.";  
 RL Cell 94:667-677(1998).  
 (7)  
 RP FUNCTION: CD2 interacts with lymphocyte function-associated  
 antigen (LFA-3) and CD48/BCM1 to mediate adhesion between T  
 cells and other cell types. CD2 is implicated in the triggering  
 of T-cells, the cytoplasmic domain is implicated in the  
 signaling function.  
 (8)  
 RP SUBUNIT: Interacts with CD2AP.  
 (9)  
 RP SUBCELLULAR LOCATION: Type I membrane protein.  
 (10)  
 RP SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 (11)  
 RP SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 (12)  
 RP This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
 DR EMBL; Y00023; CAA68258.1; -  
 DR EMBL; X06143; CAA29500.1; -  
 DR EMBL; M19807; AAA37393.1; -  
 DR EMBL; M19789; AAA37393.1; JOINED.  
 DR EMBL; M19801; AAA37393.1; JOINED.  
 DR EMBL; M19803; AAA37393.1; JOINED.  
 DR EMBL; M19805; AAA37393.1; JOINED.  
 DR EMBL; M18934; AAA37397.1; -  
 DR EMBL; BC053731; AAH53731.1; -  
 DR PIR; I49585; I49585.  
 DR HSRF; P08921; I464.  
 DR MGD; MG1:88320; Cd2.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0004872; F:receptor activity; ISS.  
 DR InterPro; IPR008424; CD2.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF05790; CD2; 1.  
 DR PROSITE; PS50835; IG\_LIKE; FALSE NEG.  
 KW Immunoglobulin domain; T-cell; Glycoprotein; Antigen; Transmembrane;  
 KW Cell adhesion; Repeat; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 344 T-CELL SURFACE ANTIGEN CD2.  
 FT DOMAIN 23 203 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 204 229 POTENTIAL.  
 FT DOMAIN 230 344 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 23 121 IG-LIKE V-TYPE.  
 FT DOMAIN 122 202 IG-LIKE C2-TYPE.  
 FT DOMAIN 276 343 PRO-RICH.  
 FT DISULFID 133 197 BY SIMILARITY.  
 FT DISULFID 140 180 BY SIMILARITY.  
 FT CARBDHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBDHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBDHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBDHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 99 98 Y -> T (IN REF. 3).  
 FT CONFLICT 128 128 M -> V (IN REF. 3 AND 4).  
 FT CONFLICT 139 139 T -> I (IN REF. 4).  
 FT CONFLICT 175 175 N -> A (IN REF. 3).  
 FT CONFLICT 175 175 N -> S (IN REF. 3).  
 FT CONFLICT 191 191 K -> N (IN REF. 2).  
 FT CONFLICT 192 192 M -> T (IN REF. 3 AND 4).  
 SQ SEQUENCE 344 AA; 38414 MW; CF012FCBD1444450 CRC64;  
 Query Match 8.1%; Score 144; DB 1; Length 344;  
 Best Local Similarity 21.4%; Pred. No. 0.00012;  
 Matches 72; Conservative 56; Mismatches 132; Indels 76; Gaps 16;  
 QY 12 YILWQLTSSAASGPVKELV-GSVGAVT--PPLSKRVQVDSIVWTFNTPLVLTIOPEGG 68  
 DB 10 FLFLFSLSGKADCRDNETIWMGLGHGITLNIPIFQMTDDIDDEVWV-----BRG 58  
 QY 69 TIIIVQNNR-----ERVDPDGGYSIKLSK-LKKNSSGIYVGIYSSSIQGPSTQEV 121  
 DB 59 TLVAEKKKKKPPFLISFTEYVLANG-SLIKIKPMKRNDSGYVWVGTNGTRLEKOLD 117  
 QY 122 LHVVEHLSPKPYKMWGLQSNKNGTCV-TNIFCCMEHGEEDVIYTWKALGOANESHNGSIL 180  
 DB 118 VRIERVSKPMI-----HMECENTLTCAVIGTDPFLKLYO--GETILNS-----L 162  
 QY 181 P---ISWEGSSDMTFCIVARNPVSRNFSPLARKLCEGAADPDSSMVLCT----- 231  
 DB 163 FQKNNSYQMTNLNAPFKCEALNPVSKESKMEV-----NCPKGLSFYTVGVAG 213  
 QY 232 -LVVLLISLVVLGFLMFLKREOEYIEKKRVDIRETPNICPHSGENTEVYTIPT 290  
 DB 214 GLLVLLVLALEF--FCICRKRKRNRKRDDELTKASRTS-----TVERGPKPHS 261  
 QY 391 NRTIKEDPANTVSVTEIIPKMEPNSHLTMPDP 326  
 DB 362 T-----PAAAGNSVALQAPPPGHILQTPGHRP 290



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RESULT 6
CD48_RAT STANDARD; PRT; 240 AA.
ID CD48_RAT
AC P10252;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE MRC OX-45 surface antigen precursor (BCM1 surface antigen) (BLAST-1)
DE (CD48).
GN CD48 OR BCM-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=89030603; PubMed=181129;
RA Killen N., Moessner R., Arvieux J., Willis A., Williams A.F.;
RT "The MRC OX-45 antigen of rat leukocytes and endothelium is in a
RT subset of the immunoglobulin superfamily with CD2, LFA-3 and
RT carcinoembryonic antigens."
RL EMBO J. 7:3087-3091(1988).
CC -1- FUNCTION: LIGAND FOR CD2. MIGHT FACILITATE INTERACTION BETWEEN
CC ACTIVATED LYMPHOCYTES. PROBABLY INVOLVED IN REGULATING T-CELL
CC ACTIVATION.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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CC -----
DR EMBL: X13016; CAA31438.1; -
DR PIR: S01299; S01299.
DR GlycosubDB: P10252; -
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003599; IG.
DR Pfam: PF00047; IG_1.
DR SMART: SM00409; IG_1.
DR PROSITE: PS50835; IG_LIKE_1.
KW Immunoglobulin domain; T-cell; Antigen; Glycoprotein; GPI-anchor;
KW Signal; Repeat; Lipoprotein.
FT CHAIN 1 22
FT SIGNAL 23 217 MRC OX-45 SURFACE ANTIGEN.
FT PROPEP 218 240 REMOVED IN MATURE FORM.
FT DOMAIN 29 127 IG-LIKE C2-TYPE 1.
FT DOMAIN 131 207 IG-LIKE C2-TYPE 2.
FT LIPID 217 217 GPI-anchor attached at serine.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 240 AA; 27680 MW; 42CBFF9947A0E437 CRC64;

Query Match 7.64; Score 134; DB 1; Length 240;
Best Local Similarity 24.64; Pred. No. 0.00053;
Matches 48; Conservative 33; Mismatches 104; Indels 10; Gaps 4;

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Db 128 VSKPAIKIEKTKNLJTSCHLRISCKVE--DQGVDTWYEDSGPFPQARNGVLEITITTH 185
QY 188 ESDMTPTCVARNPV 202
Db 186 NKSTFYTCQVSNPVS 200

RESULT 7
CD2_HUMAN STANDARD; PRT; 351 AA.
ID CD2_HUMAN
AC P06729; Q96785;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell surface antigen CD2 precursor (T-cell surface antigen
DE T11/Leu-5) (LFA-2) (LFA-3 receptor) (Erythrocyte receptor) (Rosette
DE receptor).
GN CD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND VARIANT HIS-266.
RX MEDLINE=88144486; PubMed=2894031;
RA Diamond D.J., Clayton L.K., Sayre P.H., Reinherz E.L.;
RT "Exon-intron organization and sequence comparison of human and murine
RT T11 (CD2) genes."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1615-1619(1988).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=87204137; PubMed=2437578;
RA Seed B., Aruffo A.;
RT "Molecular cloning of the CD2 antigen, the T-cell erythrocyte
RT receptor, by a rapid immunoselection procedure."
RL Proc. Natl. Acad. Sci. U.S.A. 84:3365-3369(1987).
[3]
RN SEQUENCE FROM N.A., AND VARIANT HIS-266.
RX MEDLINE=87041523; PubMed=3490670;
RA Sewell W.A., Brown M.H., Dunne J., Owen M.J., Crumpton M.J.;
RT "Molecular cloning of the human T-lymphocyte surface CD2 (T11)
RT antigen."
RL Proc. Natl. Acad. Sci. U.S.A. 83:8718-8722(1986).
[4]
RN REVISIONS.
RA Sewell W.A., Brown M.H., Dunne J., Owen M.J., Crumpton M.J.;
RL Proc. Natl. Acad. Sci. U.S.A. 84:7256-7256(1987).
[5]
RN SEQUENCE FROM N.A.
RX MEDLINE=87204283; PubMed=2883656;
RA Sayre P.H., Chang H.-C., Husey R.E., Brown N.R., Richardson N.E.,
RA Spagnoli G., Clayton L.K., Reinherz E.L.;
RT "Molecular cloning and expression of T11 cDNAs reveal a receptor-like
RT structure on human T lymphocytes."
RL Proc. Natl. Acad. Sci. U.S.A. 84:2941-2945(1987).
[6]
RN SEQUENCE FROM N.A., AND VARIANT HIS-266.
RX MEDLINE=8905055; PubMed=2901953;
RA Lang G., Worton D., Owen M.J., Sewell W.A., Brown M.H., Mason D.Y.,
RA Crumpton M.J., Kiousis D.;
RT "The structure of the human CD2 gene and its expression in transgenic
RT mice."
RL EMBO J. 7:1675-1682(1988).
[7]
RN SEQUENCE FROM N.A., AND VARIANT HIS-266.
RA Hall R.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[8]
RN SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richarde S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RL [9]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 25-206.  
RX MEDLINE=95086863; PubMed=7994575;  
RT "Crystal structure of the extracellular region of the human cell  
RT adhesion molecule CD2 at 2.5-A resolution.";  
RL Structure 2:755-766(1994).  
RL [10]  
RP STRUCTURE BY NMR OF 25-129.  
RX MEDLINE=94348865; PubMed=7915183;  
RA Bodin D.L., Jones E.Y., Harlos K., Stuart D.I., Davis S.J.,  
RT "Crystal structure of the extracellular region of the human cell  
RT adhesion molecule CD2 at 2.5-A resolution.";  
RL Structure 2:755-766(1994).  
RL [11]  
RP STRUCTURE BY NMR OF 25-129.  
RX MEDLINE=95381065; PubMed=7544493;  
RA Wysz D.F., Choi J.S., Li J., Knoppers M.H., Willis K.J.,  
RA Arulanandam A.R., Smolyar A., Reinherz E.L., Wagner G.,  
RT "Conformation and function of the N-linked glycan in the adhesion  
RT domain of human CD2.";  
RL Science 269:1273-1278(1995).  
RL [12]  
RP MUTAGENESIS.  
RX MEDLINE=8039075; PubMed=2444890;  
RA Peterson A., Seed B.,  
RT "Monoclonal antibody and ligand binding sites of the T cell  
RT erythrocyte receptor (CD2).";  
RL Nature 329:842-846(1987).  
RL [13]  
RP CD59-BINDING DATA.  
RX MEDLINE=92311658; PubMed=1377404;  
RA Hahn W.C., Menn E., Bothwell A.L.W., Sims P.J., Bieder E.F.,  
RT "Overlapping but nonidentical binding sites on CD2 for CD58 and a  
RT second ligand CD59.";  
RL Science 256:1805-1807(1992).  
CC -1- FUNCTION: CD2 interacts with lymphocyte function-associated  
CC antigen (LFA-3) and CD48/BCM1 to mediate adhesion between T  
CC cells and other cell types. CD2 is implicated in the triggering  
CC of T-cells, the cytoplasmic domain is implicated in the  
CC signaling function.  
CC -1- SUBUNIT: Interacts with CD2AP (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -1- DATABASE: NAME=PROM; NOTE=CD guide CD2 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/ProM/cd/cd2.htm".  
CC -----  
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CC -----  
DR EMBL: M16445; AAA55738.1; -  
DR EMBL: M14362; AAA55711.1; -  
DR EMBL: M16336; AAA51946.1; -  
DR EMBL: M19806; AAA53095.1; -  
DR EMBL: M19798; AAA53095.1; JOINED.  
DR EMBL: M19800; AAA53095.1; JOINED.  
DR EMBL: M19802; AAA53095.1; JOINED.  
DR EMBL: M19804; AAA53095.1; JOINED.  
DR EMBL: X07871; CAA30721.1; -  
DR EMBL: X07872; CAA30721.1; JOINED.  
DR EMBL: X07873; CAA30721.1; JOINED.  
DR EMBL: X07874; CAA30721.1; JOINED.  
DR EMBL: A1135798; CAC14840.1; -  
DR EMBL: BC03583; AAH3583.1; -  
DR PIR: A28967; RWH0C2.  
DR PDB: 1CDB; 15-OCT-94.  
DR PDB: 1HNF; 07-FEB-95.  
DR PDB: 1GYA; 08-NOV-96.  
DR PDB: 1I2Z; 20-NOV-02.  
DR GlycoSuiteDB; P06729; -  
DR Genew; HGNC:1639; CD2.  
DR MIM; 186990; -  
DR GO: GO:0005887; C:integral to plasma membrane; NAS.  
DR GO: GO:0005515; F:protein binding; IPI.  
DR GO: GO:0004872; F:receptor activity; NAS.  
DR GO: GO:000166; F:cell surface receptor linked signal transdu. .; TAS.  
DR GO: GO:0016337; F:cell-cell adhesion; NAS.  
DR GO: GO:0006917; P:induction of apoptosis; TAS.  
DR GO: GO:0045768; P:positive regulation of anti-apoptosis; NAS.  
DR GO: GO:0045580; P:regulation of T-cell differentiation; NAS.  
DR GO: GO:0042110; P:T-cell activation; TAS.  
DR InterPro; IPR008424; CD2.  
DR InterPro; IPR007110; I9-like.  
DR Pfam; PF05790; CD2; 1.  
DR PROSITE; PS50835; IG-LIKE; FALSE NEG.  
DR Immunoglobulin domain; T-cell; Glycoprotein; Antigen; Transmembrane;  
KW Cell adhesion; Repeat; Signal; Polymorphism; 3D-structure.  
FT SIGNAL 1 24  
FT CHAIN 25 351  
FT DOMAIN 25 209  
FT TRANSMEM 210 235  
FT DOMAIN 236 351  
FT DOMAIN 25 128  
FT DOMAIN 129 209  
FT DOMAIN 61 75  
FT DOMAIN 106 120  
FT DOMAIN 282 338  
FT DISULFID 139 203  
FT DISULFID 146 186  
FT CARCYHD 89 89  
FT CARCYHD 141 141  
FT CARCYHD 150 150  
FT VARIANT 266 266  
FT MUTAGEN 67 67  
FT MUTAGEN 70 70  
FT MUTAGEN 110 110  
FT MUTAGEN 111 111  
FT CONFLICT 287 287  
FT CONFLICT 339 351  
Query Match 7.5%; Score 133.5; DB 1; Length 351;  
Best Local Similarity 22.7%; Pred. No. 0.00093;  
Matches 68; Conservative 52; Mismatches 105; Indels 75; Gaps 15;  
QY 28 ELVSGVGAVPPLKS--KVGQVDSIVW--FPTNTPLVTIQEGGTLIVTQNRNRERVDF 83  
DB 32 ETWGLGQDINDLPISFQMSDDIDIDIKWKTKSDKKXIIQFRKKEKTP--KKQDYKU-F 87



FT STRAND 177 183  
 FT TURN 184 185  
 FT STRAND 186 192  
 SQ SEQUENCE 344 AA; 38414 MW; 41BAED392CE16356 CRC64;

Query Match 7.3%; Score 130; DB 1; Length 344;  
 Best Local Similarity 22.4%; Pred. No. 0.0018;  
 Matches 65; Conservative 51; Mismatches 112; Indels 62; Gaps 13;

QY 12 YILIMQLTGSAA-----SGPVKELVSGVGAATFPPLKSKVQVDSIVTNTTPLYVTIQPPG 67  
 DB 10 FLPLFSISSGADCRDGGTYWGLGH-GINLNIPTFMQTDIDBVRN-----BR 56  
 QY 68 GTTIYQNNRRERVDPPDGY-----SLKSLKKNDSGIYVGISSSLQOPSTQEVY 121  
 DB 57 GSTLVAFPRKMKKPKLKSAGFELLANGDKIKNLTFRDDSGTYVTVYSTINGRIIDKAD 116  
 QY 122 LHVYEHLSKPYTMGLQSNKNGTCV---TNLTCCMEHGBEDVIYTKALGQANESHNG 177  
 DB 117 LRILEWVSKPMIYWEK-SNATLTCEVLEGTDELKLYQCKEHL-----RSLRQKT----- 165  
 QY 178 SLTPISTMRGSDMTFICVARNPVSNFSSPIARLTCGGAADPPSSMWLCLLVLPL- 236  
 DB 166 ---MSYQNTNLRAPKCKAVNRVSQSESEMEVV-----NCPKGLPLYLVGVSA 212  
 QY 237 -LTLSPFLGLFLMFL-----KREOEYIEEK-KRVDICRETPNICPHS 278  
 DB 213 GILLVYFGALFIFCICRKKRRRRRKGELRISKASMSYVERGPK--PHS 260

RESULT 9  
 CD48 MOUSE  
 ID CD48 MOUSE STANDARD; PRT; 240 AA.  
 AC P18181;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE MRC OX-45 surface antigen precursor (BCM1 surface antigen) (BLAST-1)  
 DE (CD48) (HMA8-1).  
 GN CD48 OR BCM-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=90278362; PubMed=1693656;  
 RA Wong Y.W., Williams A.F., Kingsmore S.F., Seidin M.F.;  
 RT "Structure, expression, and genetic linkage of the mouse BCM1 (OX45  
 RT or Blast-1) antigen. Evidence for genetic duplication giving rise to  
 RT the BCM1 region on mouse chromosome 1 and the CD2/LFA3 region on  
 RT mouse chromosome 3.";  
 RL J. Exp. Med. 171:2115-2130(1990).  
 RN [2]  
 RP SEQUENCE OF 23-40.  
 RX MEDLINE=93018650; PubMed=1383383;  
 RA Kato K., Koyanagi M., Okada H., Takanahi T., Wong Y.W., Williams A.F.,  
 RT "CD48 is a counter-receptor for mouse CD2 and is involved in T cell  
 RT activation.";  
 RL J. Exp. Med. 176:1241-1249(1992).  
 CC -1- FUNCTION: LIGAND FOR CD2. MIGHT FACILITATE INTERACTION BETWEEN  
 CC ACTIVATED LYMPHOCYTES. PROBABLY INVOLVED IN REGULATING T-CELL  
 CC ACTIVATION.  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -----  
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DR EMBL; X53526; CAA37604.1; -  
 DR EMBL; X17501; CAA35542.1; -  
 DR PIR; J01043; J01043.  
 DR MGD; MG1:88339; C448.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003599; IG.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00409; IG\_1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 KW Antigen; Repeat; Signal; Immunoglobulin domain; Glycoprotein;  
 KW Lipoprotein; GPI-anchor.  
 FT SIGNAL 1 22  
 FT CHAIN 23 217  
 FT PROPEP 218 240  
 FT DOMAIN 29 125  
 FT DOMAIN 129 209  
 FT LIPID 217 217  
 FT DISULFID 151 193  
 FT CARSDHYD 32 32  
 FT CARSDHYD 38 38  
 FT CARSDHYD 70 70  
 FT CARSDHYD 136 136  
 FT CARSDHYD 186 186  
 FT CARSDHYD 203 203  
 SQ SEQUENCE 240 AA; 27383 MW; F3BF6987A9B9C71E CRC64;

Query Match 7.1%; Score 126.5; DB 1; Length 240;  
 Best Local Similarity 21.4%; Pred. No. 0.0022;  
 Matches 52; Conservative 45; Mismatches 125; Indels 21; Gaps 8;

QY 7 CTTLYIIMQLTGSAAAPVKELVSGVGAATFPPL-KSKVQVDSIVTNTTPLYVTIQP 65  
 DB 9 CLVELLILPLPTGFGQSHIDPINALTGSNVLTKIKHDPKPYKRTYLHTKNOXILEBYN 68  
 QY 66 EGGTIYQNNRRERVDPPDGYSLKSLKKNDSGIYVGISSSLQOPSTQ-EVYLHV 124  
 DB 69 YNSTITPESSEKGRVYLEENNGALHISNRKEDGIYMKV---LHETENELKITLLEV 124  
 QY 125 YEHLSPKPYTMGLQSNKNGTCVNTLTCCMEHGBEDVIYTKALGQANESHNGSLPLSW 184  
 DB 125 FDPVPRKPSIEINKTEASTDSCHLRISC--EYKQDQVDVTVWESSGPPPKSPGYLDDIV 182  
 QY 185 RWGESDMTFICVARNPVSRN-----FSSPT-LARK-LCEGAADPPSSMWLCLLVLPL 236  
 DB 183 TPONKSTFETCVSNPVSNDVYFTLPCDLARSSGVCMTA-----TWLVVTTLIIHRI 237  
 QY 237 LLS 239  
 DB 238 LIT 240

RESULT 10  
 CEAL HUMAN  
 ID CEAL HUMAN STANDARD; PRT; 526 AA.  
 AC P13688;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Carcinoembryonic antigen-related cell adhesion molecule 1 precursor  
 DE (Biliary glycoprotein 1) (BGP-1) (Antigen CD66) (CD66a antigen).  
 GN CEACAM1 OR BGP OR BGP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=88320555; PubMed=2457922;  
 RA Hinoda Y., Neumaier M., Hetta S.A., Drzeniek Z., Wagener C.,

RA Shively L., Hefta L.J.F., Shively J.E., Paxton R.J.;  
 RT "Molecular cloning of a cDNA coding bilary glycoprotein I: primary  
 RT structure of a glycoprotein immunologically crossreactive with  
 RT carcinoembryonic antigen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:6959-6963(1988).  
 RP [2]  
 RP REVISION.  
 RA Hnoda Y., Neumaier M., Hefta S.A., Dzieniek Z., Wagener C.,  
 RA Shively L., Hefta L.J.F., Shively J.E., Paxton R.J.;  
 RA Proc. Natl. Acad. Sci. U.S.A. 86:1668-1668(1989).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=9139550; PubMed=2537311;  
 RA Barnett T.R., Kretschmer A., Austen D.A., Goebel S.J., Hart J.T.,  
 RA Elting J.J., Karamer M.E.;  
 RT "Carcinoembryonic antigen: alternative splicing accounts for the  
 RT multiple mRNAs that code for novel members of the carcinoembryonic  
 RT antigen family.";  
 RL J. Cell Biol. 108:267-276(1989).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Leukocyte;  
 RX MEDLINE=91222218; PubMed=2025273;  
 RA Kuroki M., Arakawa F., Matsuo Y., Oikawa S., Nakazato H.,  
 RA Matsuo Y.;  
 RT "Three novel molecular forms of bilary glycoprotein deduced from  
 RT cDNA clones from a human leukocyte library.";  
 RL Biochem. Biophys. Res. Commun. 176:578-585(1991).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RP Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,  
 RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stijlgen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,  
 RA Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,  
 RA Liu S., Altix C., Andreise T., Frankheim M., Amico-Keller G.,  
 RA Coeffield J., Diarte S., Lucas S., Bruce R., Thomas P., Quan G.,  
 RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,  
 RA Kobayashi A., Olsen A.S., Carraro A.V.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform A).  
 CC Secreted (isoforms G, H and I).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=A;  
 CC IsoId=PI3688-1; Sequence=Displayed;  
 CC Name=G;  
 CC IsoId=PI3688-2; Sequence=VSP\_002482, VSP\_002483;  
 CC Name=H;  
 CC IsoId=PI3688-3; Sequence=VSP\_002478, VSP\_002479;  
 CC Name=I;  
 CC IsoId=PI3688-4; Sequence=VSP\_002480, VSP\_002481;  
 CC -1- DISEASE: Increased serum levels of BGP-1 are found in individuals  
 CC suffering from hepatic disorders.  
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA  
 CC family.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD66a entry;  
 CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd66a.htm".  
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DR EMBL; M69176; AAA51825.1; -;  
 DR EMBL; M72238; AAA58393.1; -;  
 DR EMBL; M72238; AAA58394.1; -;  
 DR EMBL; AC004785; AAC18434.1; -;  
 DR EMBL; AC004785; AAC18437.1; -;  
 DR EMBL; AC004785; AAC18438.1; -;  
 DR EMBL; AC004785; AAC18439.1; -;  
 DR PIR; A32164; A32164.  
 DR PIR; JH0394; JH0394.  
 DR PIR; JH0395; JH0395.  
 DR PIR; JH0396; JH0396.  
 DR Genew; HGNC:1814; CEACAM1.  
 DR MIM; 109770; -;  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO; GO:0005824; C: membrane fraction; TAS.  
 DR InterPro; IPR007110; IG-like.  
 DR Pfam; PF00047; IG\_4.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR KMW Immunoglobulin domain; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing; Pyrolydine carboxylic acid.  
 FT SIGNAL 1 34  
 FT CHAIN 35 526  
 FT FT  
 FT DOMAIN 35 428  
 FT TRANSMEM 429 452  
 FT DOMAIN 453 526  
 FT DOMAIN 35 142  
 FT DOMAIN 145 232  
 FT DOMAIN 237 317  
 FT DOMAIN 323 413  
 FT DISULFID 167 215  
 FT DISULFID 259 299  
 FT DISULFID 348 396  
 FT MOD RES 35 35  
 FT CARBOHYD 104 104  
 FT CARBOHYD 111 111  
 FT CARBOHYD 115 115  
 FT CARBOHYD 152 152  
 FT CARBOHYD 182 182  
 FT CARBOHYD 197 197  
 FT CARBOHYD 208 208  
 FT CARBOHYD 224 224  
 FT CARBOHYD 232 232  
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 FT CARBOHYD 302 302  
 FT CARBOHYD 309 309  
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 FT CARBOHYD 405 405  
 FT VARSPPLIC 320 321  
 FT VARSPPLIC 322 322  
 FT VARSPPLIC 322 526  
 FT VARSPPLIC 321 351  
 FT VARSPPLIC 352 526  
 FT VARSPPLIC 416 417  
 FT VARSPPLIC 526 526  
 FT SEQUENCE 526 AA; 57560 MW; 57560 MW; CADIB23280069AF8 CRC64;  
 SQ

Query Match 7.1%; Score 125.5; DB 1; Length 526;  
 Best Local Similarity 25.1%; Pred. No. 0.0071;  
 Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

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QY 68 GTTIVTQ-----NNRRRVDPPDGGYSKLKLNKNDGIIYVIGSSSL-QQPSIOE 119
DB 81 GVAIGGQAQTPGANGREGTI-YRNA--SILLIONVQNDGTFTLQIVISDLVNEARITQ 137
QY 120 YVLATVYHLSKPKVTMGLOSNNKNGCVNLTTCMEHGEEDVITYWKALQGANESHNGSI 179
DB 138 F--HVPBELPKPSISISNNSPEDKDAVFTC--EPEPDITLMIWI-----NNQS 184
QY 180 LPIPMW-----GSDMTFICVAR-----NVSNNFSSPIIARLCEG-----A 218
DB 185 LPVSPRLQSLNKGRTITLISVTRNDTGPYCEIQLNVSANRSDV--TLNVTGPDPTPTIS 243
QY 219 ADD----PDSMWLTLCLL--VPLLSTPLVGLFLWFLKRREROEYIEKKRVDCIRETP 272
DB 244 PSDTYRRPGANLSTSCYAAASNPPAQSWMLNGTF-----QSGTQELPI-----P 287
QY 273 NI-CPHSGENTEX--DTIHTMTITLK 296
DB 288 NITVNNSGSYTCHANNVSGCNRTTVK 314

RESULT 11
CEA6 HUMAN STANDARD; PRT; 344 AA.
ID CEA6_HUMAN
AC P40199; Q14920;
DT 01-FEB-1995 (Rel. 31, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Carcinoembryonic antigen-related cell adhesion molecule 6 precursor
DE (Normal cross-reacting antigen) (Nonspecific crossreacting antigen)
DE (CD66c antigen).
DE CEA6 OR NCA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCB1_TaxID=9606;
RN 1)
RP SEQUENCE FROM N.A.
RX MEDLINE=89122014; PubMed=3220478;
RA Barnett T., Goebel S.J., Nothdurft M.A., Eling J.J.;
RT "Carcinoembryonic antigen family: characterization of cDNAs coding
RT for NCA and CEA and suggestion of nonrandom sequence variation in
RT their conserved loop-domains.";
RL Genomics 3:59-66(1988).
RN 12)
RP SEQUENCE FROM N.A.
RX TISSUE=lung carcinoma;
RX MEDLINE=88106638; PubMed=3337731;
RA Tawaragi Y., Oikawa S., Matsuo K., Kosaki G., Nakazato H.;
RT "Primary structure of nonspecific crossreacting antigen (NCA), a
RT member of carcinoembryonic antigen (CEA) gene family, deduced from
RT cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 150:89-96(1988).
RN 13)
RP SEQUENCE FROM N.A.
RX TISSUE=Pancreas;
RX MEDLINE=23388257; PubMed=12477932;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh P.,
RA Hopkins D., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diachenko L., Marcus A., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield J.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
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RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily, CEA family.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD66c entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd66c.htm".
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL, M29541; AAA59915.1; -.
CC EMBL, M18728; AAA59907.1; -.
CC EMBL, BC005008; AAH05008.1; -.
CC Genew; HGNC:1818; CEA6.
CC MIM: 163980; -.
CC DR GO: 30.0005887; C: integral to plasma membrane; TAS.
CC DR GO: 30.0007267; P: cell-cell signaling; TAS.
CC DR GO: 30.0007165; P: signal transduction; TAS.
CC DR InterPro: IPR007110; Ig-like.
CC DR InterPro: IPR003598; Ig_c2.
CC DR Pfam: PF00047; Ig_3.
CC DR SMART; SM00408; IGC2; 1.
CC DR PROSITE; PS00835; IG_LIKE; 2.
CC KW Immunoglobulin domain; Antigen; signal; Glycoprotein; GPI-anchor;
CC Repeat; Lipoprotein.
CC FT SIGNAL 1 34
CC FT CHAIN 35 320
CC FT PROPEP 321 320
CC FT LIPID 320 340
CC FT DOMA:IN 35 142
CC FT DOMA:IN 145 232
CC FT DOMA:IN 237 314
CC FT DISULFID 167 215
CC FT DISULFID 259 299
CC FT CARBOHYD 104 104
CC FT CARBOHYD 111 111
CC FT CARBOHYD 115 115
CC FT CARBOHYD 152 152
CC FT CARBOHYD 173 173
CC FT CARBOHYD 197 197
CC FT CARBOHYD 224 224
CC FT CARBOHYD 256 256
CC FT CARBOHYD 274 274
CC FT CARBOHYD 288 288
CC FT CARBOHYD 292 292
CC FT CARBOHYD 309 309
CC FT CARBOHYD 138 138
CC FT CONFLICT 239 239
CC FT CONFLICT 344 AA; 37237 MW; 4322C5D625849F5 CRC64;
CC SQ SEQUENCE

Query Match 7.0%; Score 124.5; DB 1; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0051;
Matches 75; Conservative 35; Mismatches 110; Indels 107; Gaps 16;

QY 53 WTFTNTPLVITQ-----PEGGTTI-----VTQNR-----NRRERD----- 82
DB 28 WNPPTATLTISTEPFNVAEGKEVLLAHNLPRNRIGYSWYKGERVDSNLVGVIGTQ 87
QY 83 --FPPGGI-----SLKSLKLNKNDGIIYVIGSSSL-QQPSIOEYLVHYEHL 129
DB 88 QATPAPAYSGRETIYPNNSLLIOWTQNDTGPFTYLQVILKSLDVNEARIGQ--HVPSPILP 145
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QY 130 KPVTVMLQSNKNGTCVNTLTCMEHGEEDVYTWKALGQANESHGSLIPISRW--- 186  
 DQ 146 KPSISSNSNPVDEKQAVATC--EPVQNTYITWV-----NGSLPVSFRQLS 194  
 QY 187 -GESDFTI-----CVARNPVSRNPFSSFILARKC-----EGAADPDS 225  
 DQ 195 NGMNTLTLISVKENDAGSYCEIQNFPASNRDPVTNLVYGPDPVTPSPKANYRPGEN 254  
 QY 226 MVLLCULL--VPLLSTFVGLFLMFLKREOREYIEKKRVDCRETPV----- 274  
 DQ 255 LNTSCHAASNPPOVSWFINGTF---QOSTOLEFI-----PNTVNNSSGYM 298  
 QY 275 CPHSGETEYDTIPHTRTILKEPDANTVSTVEI 309  
 DQ 299 CQAHNSATGLNRTVTMITVSGSAPVLSAVATVGI 333

RESULT 12  
 CXAR\_HUMAN STANDARD; PRT; 365 AA.  
 AC P78310; O00694; 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-  
 DE adenovirus receptor) (hCAR) (CVB3 binding protein).  
 GN CXADR OR CAR.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteleia; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=97190109; PubMed=9036860;  
 RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,  
 RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.,  
 RA "Isolation of a common receptor for Coxsackie B viruses and  
 RT adenoviruses 2 and 5".  
 RL Science 275:1320-1323(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=97250541; PubMed=9096397;  
 RA Tomko R.P., Xu R., Philpason L.;  
 RT "hCAR and hCAR: the human and mouse cellular receptors for subgroup C  
 RT adenoviruses and group B coxsackieviruses".  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20008750; PubMed=10543405;  
 RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,  
 RA Bowles N.E.;  
 RT "Genomic organization and chromosomal localization of the human  
 RT Coxsackievirus B-adenovirus receptor gene".  
 RL Hum. Genet. 105:354-359(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Anderson C.W., Kleczkawa J., Dunn J.J., Freimuth P.;  
 RT "Sequence and expression of CXADR, the human gene for the  
 RT coxsackievirus and adenovirus receptor".  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Anderson B., Tomko R., Anderson K., Darban H., Oncu D., Mizra M.,  
 RA Solerbrant K., Schrammer E., Philpason L.;  
 RT "Putative regulatory domains in the human and mouse CAR genes".  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Cervix;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Srepleston M., Soares M.B., Bonaldo M.F., Casavant T.L., Schieff T.E.,  
 RA Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywnicki M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND  
 CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
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 DR EMBL: Y07593; CAA68868.1; -;  
 DR EMBL: U90716; AAC51234.1; -;  
 DR EMBL: AF169366; AAF05808.1; -;  
 DR EMBL: AF169360; AAF05808.1; JOINED.  
 DR EMBL: AF169361; AAF05808.1; JOINED.  
 DR EMBL: AF169362; AAF05808.1; JOINED.  
 DR EMBL: AF169363; AAF05808.1; JOINED.  
 DR EMBL: AF169364; AAF05808.1; JOINED.  
 DR EMBL: AF169365; AAF05808.1; JOINED.  
 DR EMBL: AF200465; AAF24344.1; -;  
 DR EMBL: AF242865; AAG01088.1; -;  
 DR EMBL: AF242862; AAG01088.1; JOINED.  
 DR EMBL: AF242864; AAG01088.1; JOINED.  
 DR EMBL: BC010536; AAH03684.1; -;  
 DR EMBL: BC010536; AAH03684.1; -;  
 DR PDB: 1EAW; 13-JUL-01.  
 DR PDB: 1FSW; 08-NOV-00.  
 DR PDB: 1KAC; 24-NOV-99.  
 DR Genew: HGNC:2559; CXADR.  
 DR MIM: 602621; -;  
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO: GO:0004872; F: receptor activity; TAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003598; IG\_c2.  
 DR Pfam: PF00047; Ig\_2.  
 DR SMART: SM00408; IgC2; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 2.  
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Repeat; 3D-structure.  
 FT CHAIN 1 165  
 FT SIGNAL 20 39  
 FT DOMAIN 20 237  
 FT TRANSMEM 238 258  
 FT DOMAIN 259 365  
 FT DOMAIN 20 134  
 FT DOMAIN 141 228  
 FT DISUPID 41 120  
 FT DISUPID 162 212  
 FT CARBOHYD 106 106  
 FT CARBOHYD 201 201  
 SQ SEQUENCE 365 AA; 40029 MW; ABO1C6346CB7FE64 CRC64;  
 Query Match 6.7%; Score 119.5; DB 1; Length 365;

Best Local Similarity 21.2%; Pred. No. 0.014;  
Matches 62; Conservative 47; Mismatches 124; Indels 59; Gaps 12;

QY 68 GTITVQNRNRERVPDGGVGLKSKKKNDSGIYVIGVSSLOQPSGTQSVLVHYH 127  
Db 89 GVHFTSN-----DKSGDASINVTNLQSDIGYCKVKKA---PQVANKKHLVV- 137  
QY 128 LSKPKVMTGLQSNKNGT---CVTNLTCCMEHGEEDVITYWKALGQANESHNGSLPTS 183  
Db 138 LVKPS---GARCVCOSSEISGDFKICKPKKGSLLPLQYEMKLSNDSQK-----MPTS 187  
QY 184 W-----RWGESDMTFICVARNPVSRNFSPLIARKLCEGAADDPSSMVLIC 230  
Db 188 WLAEMTSSVIVSNASSEYSGTYSCTVRNRVG---SDQCLRLD---NVVPPSNKAGLIA 240  
QY 231 LLLVPLLSFLVLGLFIMFLMKREOREYIEKKRVDICETPNICPHSENEYDPIPT 290  
Db 241 GA1IGTLALALIGLIFCCRRKRREKEYEKEVHDIRDVP--PKSRTSTARSYISGN 298  
QY 291 NRTILKEDPAN-----TVYSTV-----EIPKKNPSPSLTTPDPTPLFA 330  
Db 299 HSLSGMSPSNMEGYSKTYQNVPSDFPRTQSPPLPAKYAAPVLSMGA 350

RESULT 13  
A33\_HUMAN STANDARD; PRT; 319 AA.  
ID A33\_HUMAN  
AC Q99795;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Cell surface A33 antigen precursor (Glycoprotein A33).  
GN GPA33.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE-Colon carcinoma;  
RX MEDLINE=97165045; PubMed=9012807;  
RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,  
RA Moritz R.L., Ju G.-F., Ji H., Whitehead R.H., Groenen L.C.,  
RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,  
RA Burgess A.W.;  
RT "The human A33 antigen is a transmembrane glycoprotein and a novel  
RT member of the immunoglobulin superfamily."  
RT Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).  
RN [2]  
RP POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=97396159; PubMed=9245713;  
RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,  
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,  
RA Simpson R.J.;  
RT "Characterization of posttranslational modifications of human A33  
RT antigen, a novel palmitoylated surface glycoprotein of human  
RT gastrointestinal epithelium.";  
RL Biochem. Biophys. Res. Commun. 236:682-686(1997).  
CC -1- FUNCTION: May play a role in cell-cell recognition and signaling.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: Expressed in normal gastrointestinal  
CC epithelium and in 95% of colon cancers.  
CC -1- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED  
CC CARBOHYDRATE.  
CC -1- PTM: Palmitoylated.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

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DR EMBL: U79725; AAC50957.1; -.  
DR Genew: HGNC:4445; GPA33.  
DR MIM: 602171; -.  
DR GO: GO:0005888; C:proteoglycan integral to plasma membrane; TAS.  
DR GO: GO:0004872; F:receptor activity; TAS.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF00047; Ig\_2.  
DR SMART: SM00406; IgV\_1.  
DR PROSITE: PS50835; IG-LIKE\_2.  
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;  
KW Transmembrane; Signal; Antigen.  
FT SIGNAL 1 21  
FT CHAIN 22 319  
FT DOMAIN 22 235  
FT TRANSMEM 236 256  
FT DOMAIN 257 319  
FT DOMAIN 22 134  
FT DOMAIN 140 227  
FT DOMAIN 258 261  
FT DISULFID 43 117  
FT DISULFID 146 222  
FT DISULFID 162 211  
FT CARBOHYD 112 112  
FT CARBOHYD 200 223  
FT CARBOHYD 223 223  
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AFA5C24088 CRC64;

Query Match 6.6%; Score 116.5; DB 1; Length 319;  
Best Local Similarity 22.6%; Pred. No. 0.022;  
Matches 73; Conservative 50; Mismatches 123; Indels 77; Gaps 15;

QY 13 ILWQI-----TGSAS--GPYKELVSGVGAATPFL-----SKKYQVDSIWTPTNT 57  
Db 8 VLMTLCARVTVDAISVETPDVLRASQKSVTLPCYHTSTSSREGLIQWDKLLTH-- 65  
QY 58 TPLVITIOPEGITITQNRNRERVPDGG-----YSLKLSKLNKNDSGIYVIGVSSSLQ 113  
Db 66 TERVIVIPSPKNKYTHGELYKNRYSINNAEOSASITTDITMADNGTIESVSLMDL 125  
QY 114 QPSTOEYV-LHYEHELSPKXTMTGLQSNKNGTCVTN--LTCCMEHGEEDVITYWK--A 166  
Db 126 EGNITSRRRLVLVPSKPE--CGIEGE---TIIENNIQLTCQKSGSPTPQYSKRYNI 180  
QY 167 LGQANESHNGSLIPISRWGESDMT--FICVARNPVSRNFSPLIARKLCEGAADDPDS 224  
Db 181 INQEQPLAQPASGQVSLKNISTDTSGYICTSSNEEGTOFCNTIVAVR-----SPSM 233  
QY 225 SNVLLCLLVPLLSLFLVLGLFIMF-----LKR 252  
Db 234 NVALVYGVAGVAVALLITIGIITVCCCRGKDDNTEDKADPNREAYEBPPEQLRLSR 293  
QY 253 EROEE--YIEKKRVDICETPN 273  
Db 294 EREEDDYRQEQR-STGRESD 315

RESULT 14  
CEA5\_HUMAN STANDARD; PRT; 702 AA.  
ID CEA5\_HUMAN  
AC P06731;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Carcinoembryonic antigen-related cell adhesion molecule 5 precursor  
DE (Carcinoembryonic antigen) (CEA) (Meconium antigen 100) (CD66e  
DE antigen)  
GN CEA5 OR CEA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90258861; PubMed=2342461;  
 RA Shrawe H., Thompson J., Bona M., Hefta L.J.F., Maruya A.,  
 Haebauer M., Shively J.E., von Kleist S., Zimmermann W.;  
 RT "Cloning of the complete gene for carcinoembryonic antigen: analysis  
 of its promoter indicates a region conveying cell type-specific  
 expression.";  
 RL Mol. Cell. Biol. 10:2738-2748(1990).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88038876; PubMed=3670312;  
 RA Beauchemin N., Benchimol S., Counoyer D., Fuks A., Stanners C.P.;  
 RT "Isolation and characterization of full-length functional cDNA clones  
 for human carcinoembryonic antigen.";  
 RL Mol. Cell. Biol. 7:3221-3230(1987).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89122014; PubMed=3220478;  
 RA Barnet T., Goebel S.V., Notdurft M.A., Elting J.J.;  
 RT "Carcinoembryonic antigen family: characterization of cDNAs coding  
 for NCA and CEA and suggestion of nonrandom sequence variation in  
 their conserved loop-domains.";  
 RL Genomics 3:59-66(1988).  
 [4]  
 RP SEQUENCE OF 5-702 FROM N.A.  
 RX MEDLINE=87128144; PubMed=3814146;  
 RA Okawa S., Nakazato H., Kosaki G.;  
 RT "Primary structure of human carcinoembryonic antigen (CEA) deduced  
 from cDNA sequence.";  
 RL Biochem. Biophys. Res. Commun. 142:511-518(1987).  
 [5]  
 RP SEQUENCE OF 331-702 FROM N.A.  
 RX MEDLINE=87204247; PubMed=3033671;  
 RA Zimmermann W., Ortlieb B., Friedrich R., von Kleist S.;  
 RT "Isolation and characterization of cDNA clones encoding the human  
 carcinoembryonic antigen reveal a highly conserved repeating  
 structure.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2960-2964(1987).  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -1- TISSUE SPECIFICITY: Found in adenocarcinomas of endodermally  
 derived digestive system epithelium and fetal colon.  
 CC -1- PTM: COMPLEX IMMUNOREACTIVE GLYCOPROTEIN WITH A MW OF 180 kDa  
 CC COMPREISING 60% CARBOHYDRATE.  
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.  
 CC -1- DATABASE: NAME=CEA; NOTE=CD guide C666 entry;  
 CC WWW=http://www.ncbi.nlm.nih.gov/ncbi/prow/cd/c666.htm".  
 CC -----  
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 CC -----  
 DR EMBL; M17303; AAB59513.1; -;  
 DR EMBL; M59262; AAA62835.1; ALT SEQ.  
 DR EMBL; M59255; AAA62835.1; JOINED.  
 DR EMBL; M59256; AAA62835.1; JOINED.  
 DR EMBL; M59257; AAA62835.1; JOINED.  
 DR EMBL; M59258; AAA62835.1; JOINED.  
 DR EMBL; M59259; AAA62835.1; JOINED.  
 DR EMBL; M59260; AAA62835.1; JOINED.  
 DR EMBL; M59261; AAA62835.1; JOINED.  
 DR EMBL; M59209; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; M59710; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; M29540; AAA51967.1; -;  
 DR EMBL; X16455; CAA34474.1; -;  
 DR EMBL; M15042; AAA51963.1; -;

DR EMBL; M16234; AAA51972.1; -;  
 DR PIR; A36319; A36319.  
 DR PDB; 1E07; 04-JUL-00.  
 DR Genew; HGNC:1817; CEACAM5.  
 DR MIM; 114890; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 6.  
 DR PROSITE; PS0835; IG\_LIKE; 6.  
 KW Immunoglobulin domain; Glycoprotein; Lipoprotein; GPI-anchor;  
 KW Membrane; Signal; Repeat; 3D-structure.  
 FT SIGNAL 1 34  
 FT CHAIN 35 685  
 FT PROPER 686 702  
 FT DOMAIN 35 144  
 FT DOMAIN 146 237  
 FT DOMAIN 238 322  
 FT DOMAIN 324 415  
 FT DOMAIN 416 498  
 FT DOMAIN 502 592  
 FT DOMAIN 594 677  
 FT LIPID 685 685  
 FT CARBOHYD 104 104  
 FT CARBOHYD 115 115  
 FT CARBOHYD 152 152  
 FT CARBOHYD 182 182  
 FT CARBOHYD 197 197  
 FT CARBOHYD 204 204  
 FT CARBOHYD 208 208  
 FT CARBOHYD 246 246  
 FT CARBOHYD 256 256  
 FT CARBOHYD 274 274  
 FT CARBOHYD 288 288  
 FT CARBOHYD 292 292  
 FT CARBOHYD 309 309  
 FT CARBOHYD 330 330  
 FT CARBOHYD 351 351  
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 FT CONFLICT 320 320  
 SQ SEQUENCE 702 AA; 76795 MW; 6299AE26CDBD55C CRC64;  
 Query Match 6.5%; Score 114.5; DB 1; Length 702;  
 Best Local Similarity 21.2%; Pred. No. 0.084;  
 Matches 66; Conservative 36; Mismatches 111; Indels 99; Gaps 14;  
 68 GTTIVTQNR-----NREVPDPDGGYSKLTKKNDGIIYVGYSSSL-QQPSIOEY 120  
 81 GYVIGGQAATPGPAVSGREIIVYNA--SLLIQNIINDGTFVLHVYKSDLVNEATGCF 138  
 121 VLVHYEHLSPKPKVTMLQSNKGTCTVNLTCMEHEEDVIYTKALGQAANESHNGSL 180  
 139 --RVYELPRKPSISSNNSKRVEDKQAVATFC--EPETQATYLMVY-----NNGSL 185  
 181 PISMRW-----GSDMT-----FICVANPVSRRNFSSPIILARKL----- 214  
 186 PVSPRLQLSNGNRTTLFVNTNRDTSYKCEFTQNPVSARSBSVILNVLXGPAPTISPL 245  
 215 -----CEGAADDPDSNVLLCLLVPLLSLFLVGLFLWPKRREOREEYIEB 261  
 246 NTSYSGENMLNLSCH--AASNP-----PAGYSWFGVGTGTF-----QOSTQLFLI-- 286

Oy	262	KKRVDICRETPNI	-----CPHSGENTEDTITHTKTIKEPANTVSTVEIPKK	312
Db	287	-----PNIIVNNSGSYTCQAHNSDPTGINTRTVITVITVYAEPPKPFITSNNSNPVE	316	
Oy	313	MENPHSLTMDP	324	
Db	337	DEDAVLTCEPE	348	
	RESULT 15			
ID	CEAL_MOUSE	STANDARD;	PRT; 521 AA.	
AC	P31809;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Carcinoembryonic antigen-related cell adhesion molecule 1 precursor			
DE	(Biliary glycoprotein 1) (BGP-1) (Murine hepatitis virus receptor)			
DE	(MHV-R) (Biliary glycoprotein D).			
GN	CERCAM1 OR BGP OR BGP1 OR BGPD.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CD-1; TISSUE=Colon;			
RX	MEDLINE=93100785; PubMed=8380065;			
RA	Dveksler G.S., Diefenbach C.B., Cardellichio C.B., McCuaig K.,			
RA	Pensiero M.N.;			
RT	"Several members of the mouse carcinoembryonic antigen-related			
RT	glycoprotein family are functional receptors for the coronavirus			
RT	mouse hepatitis virus-A59."			
RT	J. Virol. 67:1-8(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c; TISSUE=Liver;			
RX	MEDLINE=92046352; PubMed=1719235;			
RA	Dveksler G.S., Pensiero M.N., Cardellichio C.B., Williams R.K.,			
RA	Jiang G.-S., Holmes K.V., Diefenbach C.W.;			
RT	"Cloning of the mouse hepatitis virus (MHV) receptor: expression in			
RT	human and hamster cell lines confers susceptibility to MHV."			
RT	J. Virol. 65:6881-6891(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=93273228; PubMed=8500759;			
RA	McCuaig K., Rosenberg M., Nedellec P., Turbide C., Beauchemin N.;			
RT	"Expression of the Bgp gene and characterization of mouse colon			
RT	biliary glycoprotein isoforms."			
RT	Gene 127:173-183(1993).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT).			
RC	STRAIN=CD-1; TISSUE=Colon;			
RX	MEDLINE=89195121; PubMed=2702644;			
RA	Beauchemin N., Turbide C., Afar D., Raymond M., Bell J.,			
RA	Stanners C.P., Fuks A.;			
RT	"A mouse analogue of the human carcinoembryonic antigen."			
RT	Cancer Res. 49:2017-2021(1989).			
RL	[5]			
RP	SEQUENCE OF 35-59.			
RX	MEDLINE=91288498; PubMed=1648219;			
RA	Williams R.K., Jiang G.-S., Holmes K.V.;			
RT	"Receptor for mouse hepatitis virus is a member of the			
RT	carcinoembryonic antigen family of glycoproteins."			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:5533-5536(1991).			
CC	-1- FUNCTION: Unknown; receptor for murine coronavirus MHV-A59.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event-Alternative splicing; Named isoforms=2;			
CC	Name=Long;			
CC	Isoid=P31809-1; Sequence=Displayed;			
CC	Name=Short;			

CC		IsoId-P31809-2; Sequence-VSP_002484, VSP_002485;
CC	-I-	SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC	-I-	SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC	-I-	SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		the Swiss Institute of Bioinformatics and the EMBL outstation
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a>
CC		or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).
CC		-----
DR	EMBL:	X67279; CAA47696.1; -
DR	EMBL:	M77196; AAA37858.1; -
DR	EMBL:	X15351; CAA33409.1; -
DR	PIR:	JC1505; WMMSR1.
DR	PIR:	JC1508; JCI508.
DR	MGI:	J347245; Ceacam1.
DR	InterPro:	IPR007110; Ig-Like.
DR	Pfam:	PF00047; Ig_3.
DR	PROSITE:	PS50835; IG_LIKE; 3.
KW		Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;
KW		Repeat; Alternative splicing; Receptor.
FT	SIGNAL	1 34
FT	CHAIN	35 521
FT		CARCINOEMBRYONIC ANTIGEN-RELATED CELL
FT	DOMAIN	35 428 ADHESION MOLECULE 1.
FT	TRANSMEM	429 447 EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	448 521 POTENTIAL.
FT	DOMAIN	35 142 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	35 142 IG-LIKE V-TYPE.
FT	DOMAIN	147 234 IG-LIKE C2-TYPE 1.
FT	DOMAIN	239 319 IG-LIKE C2-TYPE 2.
FT	DOMAIN	323 411 IG-LIKE C2-TYPE 3.
FT	DISULFID	167 217 PROBABLE.
FT	DISULFID	261 301 PROBABLE.
FT	DISULFID	346 394 PROBABLE.
FT	CARBOHYD	71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	375 375 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	455 458 GSDQ -> SGST (in isoform Short).
FT	VARSPLIC	459 521 /FTid=VSP_002484.
FT	VARSPLIC	521 521 Missing (in isoform Short).
FT	SEQUENCE	521 AA; 57015 MM; 108F71FAc47DD54E CRC64;
SO		/FTid=VSP_002485.
Query Match		6.4%; Score 113.5; DB 1; Length 521;
Best Local Similarity		26.6%; Pred. No. 0.071;
Matches	46; Conservative	25; Mismatches 69; Indels 33; Gaps 9
OY	56	NTPPLVTITQPFGGRTIVYQNNN-----RRUDFPDGGGYSLKSKLKNDNSGIYYVG I 107
DB	71	NTT---ALDKSIARVPVSNNNFTGOAYSGR-IIYSNG--SLRFQMITMKMGVYTLDM 124
OY	108	YSSSLOOPESTGEV-LHYVEHLSPKVYTMGLQSNKGVCVTNLTLCMEHGEEDEVITYMKA 166
DB	125	TDEMYRR--TDATYRFHVHPILLKPNTISNNSNPVEGDSDVSLLTCDSTYDPDNINYLWR 182
OY	167	LGOANESHSHSIIPLISRWGESDWT-----FICVARNFVSRNFSSP 208

Thu Aug 19 15:30:02 2004

us-10-063-551-46\_1.rsp

Page 21

Db 183 NGESE--GDRKLS--EGNRTLTLANTRNDTCBPYVCETRNPSVNRSDP 230

Search completed: August 18, 2004, 16:07:43  
Job time : 17 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2004, 16:04:35 ; Search time 39 Seconds  
(without alignments)  
2710.220 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772

Sequence: 1 MAGSPRCLRLIYLMQLTGS.....PHSLMPPPRUFAYENVI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 700 summaries

Database :

1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP mhc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP virus: \*  
13: SP vertebrate: \*  
14: SP unclassified: \*  
15: SP virus: \*  
16: SP bacteriaph: \*  
17: SP archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	335	4 Q9NQ25	Q9NQ25 homo sapien
2	1769	99.8	335	4 Q9NY08	Q9NY08 homo sapien
3	1392.5	78.6	328	4 Q9NY23	Q9NY23 homo sapien
4	1349	76.1	296	4 Q8N6Y8	Q8N6Y8 homo sapien
5	1160.5	65.5	228	4 Q8ND32	Q8ND32 homo sapien
6	817	46.1	333	11 Q8BH66	Q8BH66 mus musculi
7	778.5	43.9	335	11 Q8CU64	Q8CU64 mus musculi
8	773.5	43.7	335	11 Q8BRL2	Q8BRL2 mus musculi
9	769.5	43.4	335	11 Q8CU65	Q8CU65 mus musculi
10	651	36.7	300	11 Q8CU63	Q8CU63 mus musculi
11	637.5	36.0	294	11 Q91XAO	Q91XAO mus musculi
12	362.5	20.5	328	4 O15430	O15430 homo sapien
13	362.5	20.5	328	7 Q8WLP1	Q8WLP1 homo sapien
14	362.5	20.5	329	11 Q92178	Q92178 mus musculi
15	359	20.3	339	4 Q8W18	Q8W18 homo sapien
16	358	20.2	345	4 Q9UIB8	Q9UIB8 homo sapien

17	354.5	20.0	649	11 Q7TMP7	Q7TMP7 mus musculi
18	353.5	19.9	544	11 Q8C2D4	Q8C2D4 mus musculi
19	330.5	18.7	289	4 Q96A28	Q96A28 homo sapien
20	329	18.6	538	11 Q8C9E4	Q8C9E4 mus musculi
21	315.5	17.8	331	4 Q96DV0	Q96DV0 homo sapien
22	311.5	17.6	285	11 Q8BTK0	Q8BTK0 mus musculi
23	311	17.6	332	4 Q96DU3	Q96DU3 homo sapien
24	308.5	17.4	285	11 Q8VE93	Q8VE93 mus musculi
25	308	17.4	280	4 Q95660	Q95660 mus musculi
26	307.5	17.4	285	11 Q9D780	Q9D780 mus musculi
27	304	17.2	272	4 Q9UIB7	Q9UIB7 homo sapien
28	290.5	16.4	241	4 Q9UIB6	Q9UIB6 homo sapien
29	281	15.9	197	4 Q9UIT7	Q9UIT7 mus musculi
30	225.5	12.7	331	11 Q9ET40	Q9ET40 mus musculi
31	225.5	12.7	331	11 Q9ET39	Q9ET39 mus musculi
32	204.5	11.5	338	6 Q95MM6	Q95MM6 bos taurus
33	187.5	10.6	336	6 Q9GUT3	Q9GUT3 homo sapien
34	183.5	10.4	335	4 Q96GR3	Q96GR3 mus musculi
35	183	10.3	266	11 Q9CUC8	Q9CUC8 mus musculi
36	179	10.1	278	11 Q9D3G2	Q9D3G2 mus musculi
37	178	10.0	278	11 Q8R3T7	Q8R3T7 mus musculi
38	171	9.7	329	4 Q9ND2	Q9ND2 homo sapien
39	170	9.6	365	4 Q9Y288	Q9Y288 homo sapien
40	168.5	9.5	342	6 Q95L99	Q95L99 canis fami
41	167.5	9.5	342	6 Q95MM9	Q95MM9 canis fami
42	159.5	9.0	370	4 Q9BZW8	Q9BZW8 homo sapien
43	158.5	8.9	326	11 Q8CAU4	Q8CAU4 mus musculi
44	152	8.6	288	4 Q9ND26	Q9ND26 homo sapien
45	150.5	8.5	285	4 Q9P0V8	Q9P0V8 homo sapien
46	145.5	8.2	416	4 Q8N713	Q8N713 homo sapien
47	144	8.1	344	11 Q9R201	Q9R201 mus musculi
48	142	8.0	207	4 Q9HBE9	Q9HBE9 homo sapien
49	133.5	7.5	394	11 Q9R0K9	Q9R0K9 mus musculi
50	132.5	7.5	372	13 Q9RY50	Q9RY50 brachydanto
51	128.5	7.3	253	6 Q28753	Q28753 ovib sp. If
52	126.5	7.1	461	4 Q60430	Q60430 homo sapien
53	125.5	7.1	430	4 Q15600	Q15600 homo sapien
54	125.5	7.1	464	4 Q16170	Q16170 homo sapien
55	125.5	7.1	468	4 Q96CA7	Q96CA7 homo sapien
56	124.5	7.0	344	4 Q13774	Q13774 homo sapien
57	124.5	7.0	461	4 Q13854	Q13854 homo sapien
58	123.5	7.0	227	6 Q28754	Q28754 ovib sp. If
59	123	6.9	140	11 Q8BFV0	Q8BFV0 mus musculi
60	123	6.9	311	11 Q9J1M2	Q9J1M2 rattus norv
61	122.5	6.9	298	13 Q804R4	Q804R4 brachydanto
62	122.5	6.9	458	11 Q61351	Q61351 mus musculi
63	122.5	6.9	521	11 Q61352	Q61352 mus musculi
64	122	6.9	326	6 Q9N166	Q9N166 papio hamad
65	122	6.9	344	4 Q9UKV4	Q9UKV4 homo sapien
66	121.5	6.9	377	11 Q80V04	Q80V04 mus musculi
67	121.5	6.9	536	11 Q8BUE2	Q8BUE2 mus musculi
68	119.5	6.7	332	13 Q91B08	Q91B08 spinoetoides
69	118.5	6.7	520	11 Q925P2	Q925P2 mus musculi
70	115	6.5	357	13 Q90ZL5	Q90ZL5 anas platyr
71	114.5	6.5	430	4 Q8N4F1	Q8N4F1 homo sapien
72	114.5	6.5	702	4 Q8N4D0	Q8N4D0 homo sapien
73	113.5	6.4	454	11 Q91W54	Q91W54 mus musculi
74	113.5	6.4	521	11 Q925F3	Q925F3 mus musculi
75	113	6.4	373	4 Q9HEB4	Q9HEB4 mus musculi
76	113	6.4	621	11 Q811T7	Q811T7 mus musculi
77	111	6.3	372	11 Q8K1G0	Q8K1G0 rattus norv
78	110	6.2	539	6 Q8HX06	Q8HX06 sus scrofa
79	109	6.2	316	11 Q8VE98	Q8VE98 mus musculi
80	109	6.2	924	10 Q7XTP5	Q7XTP5 oryza bativ
81	108.5	6.1	365	6 Q8MWW3	Q8MWW3 bos taurus
82	108	6.1	304	11 Q9CV44	Q9CV44 mus musculi
83	108	6.1	316	11 Q7P8B4	Q7P8B4 rattus norv
84	107.5	6.1	398	11 Q07763	Q07763 mus musculi
85	107	6.0	399	11 Q95SES	Q95SES mus musculi
86	106.5	6.0	752	5 Q9XYS4	Q9XYS4 hydra atten
87	106.5	6.0	4138	5 Q811Y3	Q811Y3 plasmodium
88	106	6.0	397	11 Q9JIE0	Q9JIE0 mus musculi
89	106	6.0	897	10 Q95JY2	Q95JY2 arabidopsis

90	105.5	6.0	335	13	Q9PWR4	Q9PWR4 gallus galli	163	92.5	5.2	782	12	Q8JYB8	Q8JYB8 porcine lym
91	105.5	6.0	398	11	Q9JIE1	Q9JIE1 mus musculus	164	92.5	5.2	297	12	Q8B3U9	Q8B3U9 porcine lym
92	105	5.9	340	11	Q8B654	Q8B654 mus musculus	165	92	5.2	782	11	Q63476	Q63476 rattus norv
93	104.5	5.9	319	6	Q9TU79	Q9TU79 sus scrofa	166	92	5.2	426	4	Q60410	Q60410 homo sapien
94	104.5	5.9	1271	16	Q8A321	Q8A321 bacteroides	167	92	5.2	609	12	Q9YK07	Q9YK07 rinderpest
95	104	5.9	455	11	Q9E0L8	Q9E0L8 mus musculus	168	92	5.2	667	11	Q8CHA6	Q8CHA6 mus musculus
96	104	5.8	535	11	Q9E0T7	Q9E0T7 mus musculus	169	92	5.2	700	11	Q7TSU7	Q7TSU7 mus musculus
97	103.5	5.8	319	6	Q9TU80	Q9TU80 canis famli	170	92	5.2	822	10	Q9Z0X3	Q9Z0X3 arabidopsis
98	103.5	5.8	323	6	Q9BDP8	Q9BDP8 cercocebus	171	92	5.2	1020	11	Q8BIE6	Q8BIE6 mus musculus
99	103.5	5.8	373	11	Q8R373	Q8R373 mus musculus	172	92	5.2	1087	13	Q7ZY71	Q7ZY71 xenopus lae
100	103.5	5.8	406	4	Q8NTT8	Q8NTT8 homo sapien	173	92	5.2	2828	4	Q9MR99	Q9MR99 homo sapien
101	103	5.8	1662	13	Q8AXC7	Q8AXC7 fugu rubrip	174	91.5	5.2	160	11	Q8C254	Q8C254 mus musculus
102	103	5.8	1078	13	Q8AXC8	Q8AXC8 fugu rubrip	175	91.5	5.2	226	4	Q8NHI1	Q8NHI1 homo sapien
103	102.5	5.8	304	12	Q8JUSP1	Q8JUSP1 african swi	176	91.5	5.2	230	13	Q90Z86	Q90Z86 brachydanio
104	102.5	5.8	323	6	Q9BDM4	Q9BDM4 macaca mula	177	91.5	5.2	230	13	Q8UV30	Q8UV30 brachydanio
105	102.5	5.8	335	13	Q9YGH1	Q9YGH1 gallus galli	178	91.5	5.2	1079	12	Q9YWE6	Q9YWE6 melanoplus
106	102.5	5.8	373	11	Q9Z0S5	Q9Z0S5 mus musculus	179	91	5.1	388	4	Q8NC34	Q8NC34 homo sapien
107	102	5.8	1482	5	Q9VAY0	Q9VAY0 mus musculus	179	91	5.1	467	11	Q91VY9	Q91VY9 mus musculus
108	101.5	5.7	761	10	Q22271	Q22271 arabidopsis	180	91	5.1	467	11	Q8C6F2	Q8C6F2 mus musculus
109	100.5	5.7	259	16	Q9CFM4	Q9CFM4 lactococcus	181	91	5.1	510	6	Q9BGY6	Q9BGY6 macaca faec
110	100.5	5.7	280	13	Q8UML2	Q8UML2 ictalurus p	182	91	5.1	1496	4	Q9Z6Z6	Q9Z6Z6 homo sapien
111	100.5	5.7	323	6	Q9BDM2	Q9BDM2 cercopithec	183	91	5.1	1840	11	Q9JTI3	Q9JTI3 rattus norv
112	99.5	5.6	323	6	Q9BDM9	Q9BDM9 macaca neme	184	91	5.1	1842	4	Q8IXY3	Q8IXY3 homo sapien
113	99.5	5.6	335	13	Q9YGV5	Q9YGV5 gallus galli	185	91	5.1	2053	4	Q8WXTU7	Q8WXTU7 homo sapien
114	99.5	5.6	658	5	Q86J55	Q86J55 dictyostell	186	91	5.1	2053	4	Q8IZY4	Q8IZY4 homo sapien
115	98.5	5.6	229	11	Q8BNV8	Q8BNV8 mus musculus	187	91	5.1	2113	4	Q8TD84	Q8TD84 homo sapien
116	98.5	5.6	348	4	Q96ST1	Q96ST1 homo sapien	188	91	5.1	230	13	Q80UW9	Q80UW9 brachydanio
117	98.5	5.6	404	4	Q9GZ29	Q9GZ29 homo sapien	189	90.5	5.1	306	11	Q7TSA3	Q7TSA3 mus musculus
118	98.5	5.6	733	6	Q8SQD83	Q8SQD83 trichosurus	190	90.5	5.1	412	11	Q63611	Q63611 rattus norv
119	98.5	5.6	1227	5	Q21038	Q21038 caenorhabd	191	90.5	5.1	412	11	Q9R1B1	Q9R1B1 rattus norv
120	98.5	5.6	16215	5	Q9NFS3	Q9NFS3 drosophila	192	90.5	5.1	417	4	Q96BJ1	Q96BJ1 homo sapien
121	97.5	5.5	2772	5	Q9VAV4	Q9VAV4 drosophila	193	90.5	5.1	483	13	Q7SKX6	Q7SKX6 brachydanio
122	97.5	5.5	2776	5	Q869A0	Q869A0 drosophila	194	90.5	5.1	922	10	Q9LTU7	Q9LTU7 arabidopsis
123	97.5	5.5	2898	5	Q86829	Q86829 drosophila	195	90.5	5.1	1016	11	Q8C310	Q8C310 mus musculus
124	97	5.5	352	11	Q91W66	Q91W66 mus musculus	196	90	5.1	309	11	Q91YV7	Q91YV7 mus musculus
125	97	5.5	484	5	Q26475	Q26475 schistocerc	197	90	5.1	348	11	Q80Z24	Q80Z24 mus musculus
126	96.5	5.4	204	11	Q9JLM3	Q9JLM3 rattus norv	198	90	5.1	428	4	Q9P1W5	Q9P1W5 homo sapien
127	96.5	5.4	402	12	Q89501	Q89501 african swi	199	90	5.1	609	12	Q9MHH7	Q9MHH7 mus musculus
128	96.5	5.4	533	4	Q8NCB6	Q8NCB6 homo sapien	200	90	5.1	1431	11	Q80U60	Q80U60 mus musculus
129	96.5	5.4	534	4	Q8NBI8	Q8NBI8 homo sapien	201	89.5	5.1	756	16	Q8C1W2	Q8C1W2 streptomyce
130	96.5	5.4	1896	13	Q91AJ1	Q91AJ1 xenopus lae	202	89.5	5.1	770	16	Q89LW9	Q89LW9 bradyrhizob
131	96	5.4	339	13	Q91AZ7	Q91AZ7 spherooides	203	89.5	5.1	833	5	Q9BPQ7	Q9BPQ7 halocynthia
132	96	5.4	341	11	Q61354	Q61354 mus musculus	204	89.5	5.1	845	4	Q9H156	Q9H156 homo sapien
133	96	5.4	359	5	Q9V6C2	Q9V6C2 drosophila	205	89.5	5.1	2214	4	Q9H156	Q9H156 homo sapien
134	96	5.4	526	4	Q9H458	Q9H458 homo sapien	206	89.5	5.1	240	4	Q9BRW0	Q9BRW0 homo sapien
135	96	5.4	248	11	Q9D0T4	Q9D0T4 mus musculus	207	89	5.0	292	11	Q80T70	Q80T70 mus musculus
136	95.5	5.4	340	11	Q61349	Q61349 mus musculus	208	89	5.0	314	11	Q61238	Q61238 mus musculus
137	95.5	5.4	365	11	Q9DBU8	Q9DBU8 mus musculus	209	89	5.0	315	4	Q96DM5	Q96DM5 homo sapien
138	95.5	5.4	448	11	Q9JHL7	Q9JHL7 rattus norv	210	89	5.0	322	13	Q9PTR8	Q9PTR8 spherooides
139	95.5	5.4	458	11	Q63093	Q63093 rattus norv	211	89	5.0	325	5	Q8MKZ7	Q8MKZ7 drosophila
140	95.5	5.4	459	11	Q9JHL6	Q9JHL6 rattus norv	212	89	5.0	325	4	Q95791	Q95791 homo sapien
141	95	5.4	814	4	Q8IVU1	Q8IVU1 homo sapien	213	89	5.0	328	11	Q9Z109	Q9Z109 homo sapien
142	94.5	5.3	280	13	Q8UWK3	Q8UWK3 ictalurus p	214	89	5.0	356	11	Q64381	Q64381 mus musculus
143	94.5	5.3	286	6	Q4E535	Q4E535 bos taurus	215	89	5.0	5175	5	Q810L3	Q810L3 caenorhabd
144	94.5	5.3	379	11	Q8BLX5	Q8BLX5 mus musculus	216	89	5.0	5198	5	Q76518	Q76518 caenorhabd
145	94.5	5.3	397	11	Q8BFX8	Q8BFX8 mus musculus	217	89	5.0	271	12	Q40948	Q40948 kaposi's sa
146	94	5.3	336	6	Q8MNV8	Q8MNV8 felis silve	218	88.5	5.0	315	13	Q9DGI5	Q9DGI5 gallus galli
147	94	5.3	344	11	Q9R067	Q9R067 rattus norv	219	88.5	5.0	325	13	Q8UWK3	Q8UWK3 ictalurus p
148	94	5.3	419	4	Q96QL5	Q96QL5 homo sapien	220	88.5	5.0	344	13	Q93242	Q93242 gallus galli
149	94	5.3	828	11	Q8C8T7	Q8C8T7 mus musculus	221	88.5	5.0	532	4	Q8WVW6	Q8WVW6 homo sapien
150	93.5	5.3	358	11	Q9R066	Q9R066 rattus norv	222	88.5	5.0	534	4	Q96S42	Q96S42 homo sapien
151	93	5.2	316	4	Q9BXK1	Q9BXK1 homo sapien	223	88.5	5.0	554	5	Q9MAR3	Q9MAR3 drosophila
152	93	5.2	339	9	Q9V5T7	Q9V5T7 drosophila	224	88.5	5.0	583	11	Q8CDN5	Q8CDN5 mus musculus
153	93	5.2	342	13	Q91B00	Q91B00 spherooides	225	88.5	5.0	1081	5	Q8T4N8	Q8T4N8 penaeus sem
154	93	5.2	752	13	Q9DGN6	Q9DGN6 gallus galli	226	88	5.0	324	11	Q7TMH2	Q7TMH2 mus musculus
155	93	5.2	793	11	Q70Z46	Q70Z46 mus musculus	227	88	5.0	329	6	Q9TFP2	Q9TFP2 canis famli
156	93	5.2	813	11	Q8BQO3	Q8BQO3 mus musculus	228	88	5.0	337	13	Q9IAZ4	Q9IAZ4 spherooides
157	93	5.2	1788	13	Q91AJ0	Q91AJ0 xenopus lae	229	88	5.0	339	13	Q91B09	Q91B09 spherooides
158	92.5	5.2	160	11	Q8C239	Q8C239 mus musculus	230	88	5.0	343	11	Q8R4Y0	Q8R4Y0 mus musculus
159	92.5	5.2	485	13	Q80UW5	Q80UW5 brachydanio	231	88	5.0	422	17	Q58124	Q58124 pyrococcus
160	92.5	5.2	544	13	Q7Z285	Q7Z285 brachydanio	232	88	5.0	457	11	Q61396	Q61396 mus musculus
161	92.5	5.2	760	16	Q8EBB5	Q8EBB5 shewanella	233	88	5.0	530	11	Q80XJ5	Q80XJ5 mus musculus
162	92.5	5.2	761	10	Q9C963	Q9C963 arabidopsis	234	88	5.0	699	11	Q61042	Q61042 mus musculus

236	88	5.0	837	16	08G518	08G518 bifidobacte	309	85.5	4.8	2115	5	08IE55	08IE55 plasmidium
237	88	5.0	986	13	08UVR9	08UVR9 fugu rubrip	310	85.5	4.8	2491	4	096PT5	096PT5 homo sapien
238	88	5.0	1379	5	08I3S7	08I3S7 plasmidium	311	85.5	4.8	2491	4	096PT5	096PT5 homo sapien
239	88	5.0	1945	4	08I2D2	08I2D2 homo sapien	312	85.5	4.8	2588	11	088491	088491 mus musculu
240	88	5.0	1985	4	09Y4D7	09Y4D7 homo sapien	313	85	4.8	224	3	0870G0	0870G0 podopora a
241	88	5.0	3007	4	014215	014215 homo sapien	314	85	4.8	280	13	08UWL1	08UWL1 itcalurus p
242	87.5	4.9	276	12	064861	064861 human adeno	315	85	4.8	332	16	08EXS1	08EXS1 leptospira
243	87.5	4.9	276	12	098822	098822 human adeno	316	85	4.8	375	2	093GD6	093GD6 desulfobivr
244	87.5	4.9	325	6	002838	002838 sus scrofa	317	85	4.8	379	11	0880U9	0880U9 mus musculu
245	87.5	4.9	403	11	08VE47	08VE47 mus musculu	318	85	4.8	583	6	09BHI3	09BHI3 bos taurus
246	87.5	4.9	487	13	072H27	072H27 gallus gall	319	85	4.8	684	5	0211J8	0211J8 caenorhabd1
247	87.5	4.9	583	11	035112	035112 rattus norv	320	85	4.8	709	6	09XSJ2	09XSJ2 sus scrofa
248	87.5	4.9	583	11	08R2T0	08R2T0 mus musculu	321	85	4.8	875	11	091ZY7	091ZY7 mus musculu
249	87.5	4.9	652	12	089703	089703 caseava vei	322	85	4.8	1376	12	08A2Z3	08A2Z3 porcine lym
250	87.5	4.9	1087	13	09PUF6	09PUF6 gallus gall	323	85	4.8	1598	4	09P214	09P214 homo sapien
251	87.5	4.9	2307	12	080IV2	080IV2 chellier-lik	324	85	4.8	1723	11	08CHB2	08CHB2 mus musculu
252	87.5	4.9	2340	11	064736	064736 mus musculu	325	85	4.8	2487	6	09N1T0	09N1T0 ornithorhyn
253	87.5	4.9	4162	13	098918	098918 gallus gall	326	84.5	4.8	280	16	089PD0	089PD0 clostridium
254	87.5	4.9	4283	11	098RV0	098RV0 rattus norv	327	84.5	4.8	303	4	09UKJ1	09UKJ1 homo sapien
255	87.5	4.9	18074	5	0917U4	0917U4 drosoephila	328	84.5	4.8	355	4	0723B1	0723B1 mus musculu
256	87	4.9	229	11	09R121	09R121 rattus norv	329	84.5	4.8	394	11	09D0G8	09D0G8 mus musculu
257	87	4.9	291	11	08C6C3	08C6C3 mus musculu	330	84.5	4.8	656	10	004533	004533 arabidopsis
258	87	4.9	326	11	08C191	08C191 mus musculu	331	84.5	4.8	798	5	086K66	086K66 dictyostell
259	87	4.9	341	11	061353	061353 mus musculu	332	84.5	4.8	840	16	07VQI2	07VQI2 candidatus
260	87	4.9	403	11	09CYD6	09CYD6 mus musculu	333	84.5	4.8	1164	17	08PX58	08PX58 methanosarc
261	87	4.9	415	11	08C6X8	08C6X8 mus musculu	334	84.5	4.8	1508	17	08BVT0	08BVT0 methanosarc
262	87	4.9	491	11	08E0Z8	08E0Z8 mus musculu	335	84.5	4.8	4311	6	07YOK5	07YOK5 canis famli
263	87	4.9	514	11	08BH18	08BH18 mus musculu	336	84	4.7	262	13	09PTR7	09PTR7 spiroeroides
264	87	4.9	521	6	046651	046651 oryctolagus	337	84	4.7	333	13	09IB04	09IB04 spiroeroides
265	87	4.9	522	16	08F7F1	08F7F1 leptospira	338	84	4.7	343	11	08BYS4	08BYS4 mus musculu
266	87	4.9	873	11	08CD46	08CD46 mus musculu	339	84	4.7	403	16	08BNX5	08BNX5 oceanobacti
267	87	4.9	1501	11	07TT17	07TT17 mus musculu	340	84	4.7	556	13	072ZU8	072ZU8 brachydantio
268	87	4.9	1904	11	064699	064699 mus musculu	341	84	4.7	593	3	08NKB1	08NKB1 emericella
269	87	4.9	2673	4	096SC3	096SC3 homo sapien	342	84	4.7	775	6	097754	097754 oryctolagus
270	86.5	4.9	293	13	08XN8	08XN8 cyprinus ca	343	84	4.7	800	10	08H329	08H329 oryza sativ
271	86.5	4.9	313	11	035531	035531 rattus norv	344	84	4.7	810	5	08T3J2	08T3J2 drosoephila
272	86.5	4.9	324	13	091AY9	091AY9 spiroeroides	345	84	4.7	811	5	09VKS4	09VKS4 drosoephila
273	86.5	4.9	354	4	08NAO3	08NAO3 homo sapien	346	84	4.7	812	5	08M257	08M257 drosoephila
274	86.5	4.9	474	6	P79355	P79355 fellis alive	347	84	4.7	851	17	09UX76	09UX76 sulfoblus
275	86.5	4.9	528	16	09RTP5	09RTP5 delinococcus	348	84	4.7	880	5	P91643	P91643 drosoephila
276	86.5	4.9	650	16	088BN9	088BN9 pseudomonas	349	84	4.7	992	10	07XTP4	07XTP4 oryza sativ
277	86.5	4.9	846	11	0810C0	0810C0 mus musculu	350	84	4.7	1062	12	0997A4	0997A4 american pl
278	86	4.9	259	4	09Y5B2	09Y5B2 homo sapien	351	84	4.7	1193	5	09VOM1	09VOM1 drosoephila
279	86	4.9	280	13	08UWK1	08UWK1 itcalurus p	352	84	4.7	1499	13	090815	090815 gallus gall
280	86	4.9	339	13	091AZ1	091AZ1 spiroeroides	353	83.5	4.7	284	6	09GLJ3	09GLJ3 bos taurus
281	86	4.9	354	12	098VN1	098VN1 human herpe	354	83.5	4.7	289	11	08K3J3	08K3J3 meriones un
282	86	4.9	428	4	09BRW2	09BRW2 homo sapien	355	83.5	4.7	315	17	050082	050082 pyrococcus
283	86	4.9	487	16	082N16	082N16 streptomyce	356	83.5	4.7	392	5	076708	076708 caenorhabd1
284	86	4.9	487	16	082M13	082M13 streptomyce	357	83.5	4.7	408	11	091WP1	091WP1 mus musculu
285	86	4.9	545	5	09VCT4	09VCT4 atrosophila	358	83.5	4.7	408	11	08BVP6	08BVP6 mus musculu
286	86	4.9	667	10	09MAJ5	09MAJ5 arabidopsis	359	83.5	4.7	408	11	08K094	08K094 mus musculu
287	86	4.9	731	6	08SP16	08SP16 macropus eu	360	83.5	4.7	515	4	096R80	096R80 homo sapien
288	86	4.9	885	10	08L3R3	08L3R3 arabidopsis	361	83.5	4.7	515	4	096PJ5	096PJ5 homo sapien
289	86	4.9	885	10	08L3Y7	08L3Y7 arabidopsis	362	83.5	4.7	528	5	P91670	P91670 drosoephila
290	86	4.9	885	10	081401	081401 arabidopsis	363	83.5	4.7	577	16	081H34	081H34 bacillus ce
291	86	4.9	885	10	081GPR	081GPR arabidopsis	364	83.5	4.7	546	16	0899Y4	0899Y4 clostridium
292	86	4.9	1187	13	098TF0	098TF0 cyprinus ca	365	83.5	4.7	1059	13	09DB49	09DB49 brachydantio
293	86	4.9	1327	4	015070	015070 homo sapien	366	83.5	4.7	1463	11	055124	055124 mus musculu
294	86	4.9	18412	13	072Z61	072Z61 brachydantio	367	83.5	4.7	1501	11	09QW00	09QW00 rattus sp.
295	85.5	4.8	326	4	09UPK8	09UPK8 homo sapien	368	83.5	4.7	1556	16	083NF7	083NF7 terephryma
296	85.5	4.8	336	4	075237	075237 homo sapien	369	83.5	4.7	1602	12	09J5C2	09J5C2 fowlpox vix
297	85.5	4.8	333	4	075238	075238 homo sapien	370	83.5	4.7	1663	11	064605	064605 rattus norv
298	85.5	4.8	335	4	075237	075237 homo sapien	371	83	4.7	151	6	07Y589	07Y589 sus scrofa
299	85.5	4.8	333	11	07TNZ6	07TNZ6 rattus norv	372	83	4.7	231	4	08WY6	08WY6 homo sapien
300	85.5	4.8	650	4	08NA84	08NA84 homo sapien	373	83	4.7	234	11	061401	061401 mus musculu
301	85.5	4.8	657	2	093D79	093D79 bacillus th	374	83	4.7	273	4	09NOD3	09NOD3 homo sapien
302	85.5	4.8	789	2	045793	045793 bacillus th	375	83	4.7	281	11	08CUE8	08CUE8 mesocricetu
303	85.5	4.8	789	2	069270	069270 bacillus th	376	83	4.7	339	11	09JTK5	09JTK5 mus musculu
304	85.5	4.8	789	2	045792	045792 bacillus th	377	83	4.7	339	13	091AZ2	091AZ2 spiroeroides
305	85.5	4.8	789	2	093821	093821 bacillus th	378	83	4.7	369	2	093EW5	093EW5 desulfobivr
306	85.5	4.8	1101	10	09FWL8	09FWL8 oryza sativ	379	83	4.7	373	17	08UT74	08UT74 methanosarc
307	85.5	4.8	1101	10	07XDJ5	07XDJ5 oryza sativ	380	83	4.7	401	6	008835	008835 cercopithec
308	85.5	4.8	1354	5	09VIC7	09VIC7 drosoephila	381	83	4.7	437	13	090W14	090W14 gallus gall

382	83	4.7	514	4	Q9H0C3	Q9H0C3 homo sapien	455	81.5	4.6	473	16	Q8ZQD1	Q8zqdi salmonella
383	83	4.7	538	13	Q9DFU0	Q9dfu0 sparus aura	456	81.5	4.6	502	2	Q842D1	Q842d1 escherichia
384	83	4.7	577	11	Q9D221	Q9d221 mus musculus	457	81.5	4.6	504	2	Q8N441	Q8n441 homo sapien
385	83	4.7	885	10	Q8L600	Q8l6q0 arabidopsis	458	81.5	4.6	504	4	Q9H4D7	Q9h4d7 homo sapien
386	83	4.7	885	10	Q8L6P9	Q8l6p9 arabidopsis	459	81.5	4.6	524	2	Q0S012	Q0s012 shigella so
387	83	4.7	885	10	Q8L6P7	Q8l6p7 arabidopsis	460	81.5	4.6	606	5	Q9VMN6	Q9vmn6 drosophila
388	83	4.7	925	5	Q9U4B4	Q9u4e4 caenorhabdi	461	81.5	4.6	677	16	Q8A3Q5	Q8a3q5 bacteroides
389	83	4.7	925	5	Q9UB95	Q9ub95 caenorhabdi	462	81.5	4.6	708	10	Q9M1P4	Q9m1p4 arabidopsis
390	83	4.7	925	5	Q9UB94	Q9ub94 caenorhabdi	463	81.5	4.6	779	16	Q8AAG1	Q8aag1 bacteroides
391	83	4.7	925	5	Q44191	Q44191 caenorhabdi	464	81.5	4.6	824	16	Q8A3C4	Q8a3c4 bacteroides
392	83	4.7	1106	5	Q8LBR5	Q8lbr5 plasmodium	465	81.5	4.6	873	13	Q4Z5S5	Q4z5s5 xenopus lae
393	83	4.7	2421	6	Q95M11	Q95m11 lemur catta	466	81.5	4.6	968	5	Q9VR40	Q9vr40 drosophila
394	83	4.7	2429	3	Q06116	Q06116 saccharomyc	467	81.5	4.6	1187	13	Q932B4	Q932b4 figu rubrip
395	82.5	4.7	155	4	Q96P81	Q96p81 homo sapien	468	81.5	4.6	1194	3	Q93962	Q93962 glomus vers
396	82.5	4.7	230	13	Q8UV76	Q8uv76 brachydantio	469	81.5	4.6	1194	11	Q7TPV3	Q7tpv3 mus musculus
397	82.5	4.7	270	4	Q9HS40	Q9hs40 sus scrofa	470	81.5	4.6	1214	4	Q7S054	Q7s054 homo sapien
398	82.5	4.7	270	4	Q9HS40	Q9hs40 sus scrofa	471	81.5	4.6	1596	4	Q9HCL6	Q9hcl6 homo sapien
399	82.5	4.7	319	11	Q9Z2D5	Q9z2d5 mus musculus	472	81.5	4.6	2212	4	Q9MHN3	Q9mhn3 homo sapien
400	82.5	4.7	330	11	P97269	P97269 cavia porce	473	81.5	4.6	2284	5	Q815Y7	Q815y7 plasmodium
401	82.5	4.7	373	10	Q96SH0	Q96sh0 arabidopsis	474	81.5	4.6	6620	4	Q96AA2	Q96aa2 homo sapien
402	82.5	4.7	378	10	Q8L4Y2	Q8l4y2 arabidopsis	475	81.5	4.6	149	5	Q86L22	Q86l22 dictyosteli
403	82.5	4.7	393	10	Q9C9P8	Q9c9p8 arabidopsis	476	81	4.6	151	6	Q867B8	Q867b8 sus scrofa
404	82.5	4.7	446	3	Q8NK03	Q8nk03 emericella	477	81	4.6	252	4	Q95781	Q95781 homo sapien
405	82.5	4.7	462	10	Q8LBP4	Q8lbp4 arabidopsis	478	81	4.6	272	7	Q861J5	Q861j5 equus caball
406	82.5	4.7	576	17	Q8TQX0	Q8tqx0 methanosarc	479	81	4.6	291	11	Q8CD40	Q8cd40 mus musculus
407	82.5	4.7	833	5	Q9VHG1	Q9vhg1 drosophila	480	81	4.6	326	13	Q91AY7	Q91ay7 spherooides
408	82.5	4.7	840	2	Q84B27	Q84b27 spiroplasma	481	81	4.6	330	16	Q87W83	Q87w83 pseudomonas
409	82.5	4.7	840	2	Q84B26	Q84b26 spiroplasma	482	81	4.6	338	4	Q81V49	Q81v49 homo sapien
410	82.5	4.7	994	5	Q96167	Q96167 plasmodium	483	81	4.6	374	10	Q43741	Q43741 bromheadia
411	82.5	4.7	1028	4	Q9U052	Q9uq52 homo sapien	484	81	4.6	423	5	Q9UAG6	Q9uag6 dictyosteli
412	82.5	4.7	1241	16	Q83GQ1	Q83gq1 tirophetima	485	81	4.6	438	11	Q920C3	Q920c3 mus musculus
413	82.5	4.7	1319	5	Q9BJF3	Q9bjf3 oxytricha t	486	81	4.6	451	16	Q8DDA0	Q8dda0 vibrio vuln
414	82.5	4.7	4256	6	Q8MJF3	Q8mjf3 canis famli	487	81	4.6	507	5	Q9U319	Q9u319 caenorhabdi
415	82.5	4.7	4650	4	Q15598	Q15598 homo sapien	488	81	4.6	521	6	Q46634	Q46634 canis famli
416	82.5	4.7	26926	4	Q8WXB3	Q8wb23 homo sapien	489	81	4.6	624	10	Q9AAX9	Q9aax9 arabidopsis
417	82.5	4.7	26926	4	Q10466	Q10466 homo sapien	490	81	4.6	643	10	Q7Y231	Q7y231 arabidopsis
418	82.5	4.7	34350	4	Q8W422	Q8w422 homo sapien	491	81	4.6	769	16	Q971S9	Q971s9 clostridium
419	82.5	4.7	151	6	Q7Y688	Q7y688 sus scrofa	492	81	4.6	937	16	Q8G4P3	Q8g4p3 bifidobacte
420	82	4.6	184	16	Q7VM71	Q7vm71 haemophilus	493	81	4.6	1196	13	Q9M7F1	Q9m7f1 cyrinus ca
421	82	4.6	308	6	Q9SK99	Q9sk99 macaca fasc	494	81	4.6	1220	3	Q9P3A8	Q9p3a8 schizosacch
422	82	4.6	324	4	Q8NBV8	Q8nbv8 homo sapien	495	81	4.6	1898	11	Q64504	Q64504 r proteacth
423	82	4.6	326	4	Q8NC17	Q8nc17 homo sapien	496	81	4.6	1901	16	Q7U170	Q7u170 rhodospirilli
424	82	4.6	337	4	Q96107	Q96107 homo sapien	497	81	4.6	2219	16	Q88W19	Q88w19 lactobacilli
425	82	4.6	331	13	Q91B01	Q91b01 spherooides	498	81	4.6	2402	2	Q9AER7	Q9aer7 staphylococ
426	82	4.6	409	16	Q814M1	Q814m1 bacillus ce	499	80.5	4.5	261	13	Q9M6V1	Q9m6v1 gallus gall
427	82	4.6	412	6	Q8HY14	Q8hy14 crytocolagus	500	80.5	4.5	270	4	Q9UMT1	Q9umt1 homo sapien
428	82	4.6	444	10	Q8S917	Q8s917 arabidopsis	501	80.5	4.5	290	16	Q8CRP9	Q8crp9 streptilococ
429	82	4.6	567	13	P78721	P78721 orpinomyces	502	80.5	4.5	371	16	Q816T2	Q816t2 bacillus ce
430	82	4.6	634	3	Q9P8L1	Q9p8l1 carassius a	503	80.5	4.5	376	10	Q94B08	Q94b08 arabidopsis
431	82	4.6	648	11	Q9EPF1	Q9epf1 crytlococcu	504	80.5	4.5	376	10	Q23195	Q23195 arabidopsis
432	82	4.6	709	6	Q9XSJ1	Q9xjs1 mus musculus	505	80.5	4.5	388	11	Q8R464	Q8r464 mus musculus
433	82	4.6	709	11	Q08702	Q08702 rattus norv	506	80.5	4.5	472	11	Q81I88	Q81i88 mus musculus
434	82	4.6	727	11	Q70376	Q70376 rattus norv	507	80.5	4.5	473	16	Q8Z809	Q8z809 salmonella
435	82	4.6	757	11	Q70482	Q70482 rattus norv	508	80.5	4.5	475	11	Q6Z056	Q6z056 mus musculus
436	82	4.6	785	11	Q9QZF9	Q9qzf9 rattus norv	509	80.5	4.5	498	16	Q886D9	Q886d9 pseudomonas
437	82	4.6	795	4	Q8ND69	Q8nd69 mus musculus	510	80.5	4.5	540	16	Q8XB55	Q8xb55 escherichia
438	82	4.6	890	4	Q8EYF3	Q8eyf3 homo sapien	511	80.5	4.5	546	11	Q80X70	Q80x70 mus musculus
439	82	4.6	890	4	Q8EYF3	Q8eyf3 homo sapien	512	80.5	4.5	548	11	Q99NB3	Q99nb3 mus musculus
440	82	4.6	1038	11	Q8CH43	Q8ch43 mus musculus	513	80.5	4.5	556	16	Q8DEW4	Q8dew4 vibrio vuln
441	82	4.6	1166	11	Q80VPO	Q80vp0 mus musculus	514	80.5	4.5	564	13	Q7ZU00	Q7zu00 brachydantio
442	82	4.6	2136	10	Q8RYW8	Q8ryw8 cryza sativ	515	80.5	4.5	602	4	Q86YJ9	Q86yj9 homo sapien
443	82	4.6	2940	5	Q8IHP9	Q8lhp9 plasmodium	516	80.5	4.5	662	4	Q60926	Q60926 homo sapien
444	82	4.6	3173	16	Q882M6	Q882m6 pseudomonas	517	80.5	4.5	707	10	Q7XN77	Q7xnt7 cryza sativ
445	82	4.6	5636	4	Q96RW7	Q96rw7 homo sapien	518	80.5	4.5	721	3	Q13479	Q13479 aspergillus
446	81.5	4.6	329	13	Q91AV1	Q91av1 xenopus lae	519	80.5	4.5	739	6	Q865P2	Q865p2 crytocolagus
447	81.5	4.6	329	13	Q91AY6	Q91aye spherooides	520	80.5	4.5	789	2	Q88S25	Q88s25 bacillus th
448	81.5	4.6	340	13	Q90Z89	Q90z89 brachydantio	521	80.5	4.5	823	10	Q39594	Q39594 chlamydomon
449	81.5	4.6	352	4	Q15403	Q15403 homo sapien	522	80.5	4.5	932	11	Q7TQ14	Q7tq14 rattus norv
450	81.5	4.6	352	4	Q08266	Q08266 homo sapien	523	80.5	4.5	976	13	Q8JFR5	Q8jfr5 brachydantio
451	81.5	4.6	355	10	Q65493	Q65493 arabidopsis	524	80.5	4.5	976	13	Q918V6	Q918v6 gallus gall
452	81.5	4.6	411	4	Q15228	Q15228 homo sapien	525	80.5	4.5	1146	13	Q918V6	Q918v6 gallus gall
453	81.5	4.6	411	4	Q15228	Q15228 homo sapien	526	80.5	4.5	1202	11	Q80U33	Q80u33 mus musculus
454	81.5	4.6	438	13	Q7T028	Q7t028 xenopus lae	527	80.5	4.5	1465	4	Q7Z3Y2	Q7z3y2 homo sapien





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674 77.5 4.4 128 4 Q86UW2 Q86UW2 homo sapien
675 77.5 4.4 172 5 Q196Z7 Q196Z7 caenorhabdi
676 77.5 4.4 186 5 Q8WV99 Q8WV99 ixodes scap
677 77.5 4.4 214 16 Q99VY1 Q99VY1 staphyloccc
678 77.5 4.4 258 4 Q9H563 Q9H563 homo sapien
679 77.5 4.4 284 4 Q9N542 Q9N542 homo sapien
680 77.5 4.4 294 11 Q8K1Z5 Q8K1Z5 mus musculu
681 77.5 4.4 300 11 Q9JHY1 Q9JHY1 rattus norv
682 77.5 4.4 324 10 Q940M5 Q940M5 arabidopsi
683 77.5 4.4 326 13 Q91A23 Q91A23 spherooids
684 77.5 4.4 345 8 Q9G9W4 Q9G9W4 teleogryllu
685 77.5 4.4 345 8 Q9G9W3 Q9G9W3 teleogryllu
686 77.5 4.4 351 2 Q9ADX7 Q9ADX7 agrobacteri
687 77.5 4.4 356 13 Q8AXL7 Q8AXL7 oncorhynch
688 77.5 4.4 360 16 Q7VWZ7 Q7VWZ7 prochloroco
689 77.5 4.4 371 16 Q81K07 Q81K07 bacillus an
690 77.5 4.4 425 3 Q96VU0 Q96VU0 amanita mus
691 77.5 4.4 428 16 Q8F7J7 Q8F7J7 leptospira
692 77.5 4.4 433 11 Q55054 Q55054 mus musculu
693 77.5 4.4 460 5 Q7YTA8 Q7YTA8 bombyx mori
694 77.5 4.4 476 11 Q9CU34 Q9CU34 mus musculu
695 77.5 4.4 536 16 Q7UZH7 Q7UZH7 prochloroco
696 77.5 4.4 539 10 Q9FX24 Q9FX24 arabidopsi
697 77.5 4.4 589 10 Q8RZH3 Q8RZH3 oryza sativ
698 77.5 4.4 591 16 Q911K8 Q911K8 pseudomonas
699 77.5 4.4 717 16 Q8U7P9 Q8U7P9 agrobacteri
700 77.5 4.4 735 10 Q9FG24 Q9FG24 arabidopsi
```

## ALIGNMENTS

## RESULT 1

Q9NQ25 PRELIMINARY; PRT; 335 AA.

```
AC Q9NQ25;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BA404F10.4 (Novel LY9 (Lymphocyte antigen 9) like protein) (NK cell
DE receptor) (Membrane protein FOAP-12) (CD2-like receptor activating
DE cytotoxic cells) .
GN BA404F10.4 OR CSI.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bates K.;
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Boles K.S., Mathew P.A. Sr.;
RT "Cloning of a new member of the CD2 subset of receptors expressed on
RT NK cells.";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RA Fujii Y., Takayama K., Tsuritani K., Yajima Y., Amemiya T., Ukai Y.,
RA Naito K., Kawaguchi A.;
RT "Homo sapiens mRNA for FOAP-12 protein, complete cds.";
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;
RT "Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a SAP-
RT Independent Receptor of the CD2 Family.";
RT J. Immunol. 167:0-0(2001) .
DR EMBL: AL121985; CAC00579.1; -
DR EMBL: AF291815; AAK11549.1; -
DR EMBL: AB027233; BAB61022.1; -
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DR EMBL: AF390894; AAL26989.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR003599; IG.
DR SMART: IPR007110; IG-like.
DR SMART: SM00409; IG, 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR RECEPTOR.
SQ SEQUENCE 335 AA; 37421 MW; D09ABCF74BE8D4 CRC64;
```

Query Match 100.0%; Score 1772; DB 4; Length 335;  
Best Local Similarity 100.0%; Pred. No. 6.5e-159;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAGSPFTCLTLIYIQLTGSAAAGPVKEIVSGAVTFPLSKYKQVDSIWTNTTPTL 60
DB 1 MAGSPFTCLTLIYIQLTGSAAAGPVKEIVSGAVTFPLSKYKQVDSIWTNTTPTL 60
QY 61 VTIOPEGGTTIVTQNRNRRVDFPDGYSLSKLKSKNDGSIYVGIYSSSIQOPSTOY 120
DB 61 VTIOPEGGTTIVTQNRNRRVDFPDGYSLSKLKSKNDGSIYVGIYSSSIQOPSTOY 120
QY 121 VLAHYEHLSPKRVMTGLQSNKNGTCVTNLTCMEHGEDVITYTKALQAAHSHNGSL 180
DB 121 VLAHYEHLSPKRVMTGLQSNKNGTCVTNLTCMEHGEDVITYTKALQAAHSHNGSL 180
QY 122 VLAHYEHLSPKRVMTGLQSNKNGTCVTNLTCMEHGEDVITYTKALQAAHSHNGSL 180
DB 122 VLAHYEHLSPKRVMTGLQSNKNGTCVTNLTCMEHGEDVITYTKALQAAHSHNGSL 180
QY 181 PISPMWGESDMTFICVARNPVSRNFSPIARKLCEGAADDPDSMTLLCLLVPLLSL 240
DB 181 PISPMWGESDMTFICVARNPVSRNFSPIARKLCEGAADDPDSMTLLCLLVPLLSL 240
QY 181 PISPMWGESDMTFICVARNPVSRNFSPIARKLCEGAADDPDSMTLLCLLVPLLSL 240
DB 181 PISPMWGESDMTFICVARNPVSRNFSPIARKLCEGAADDPDSMTLLCLLVPLLSL 240
QY 241 FVLGLFLWFLKREOEYIEKKRVDICRETPNICPHSGENTYDTIPIHNTTIKEDPA 300
DB 241 FVLGLFLWFLKREOEYIEKKRVDICRETPNICPHSGENTYDTIPIHNTTIKEDPA 300
QY 241 FVLGLFLWFLKREOEYIEKKRVDICRETPNICPHSGENTYDTIPIHNTTIKEDPA 300
DB 241 FVLGLFLWFLKREOEYIEKKRVDICRETPNICPHSGENTYDTIPIHNTTIKEDPA 300
QY 301 NTVYSTVEIPKKEHPHSLTTPDTPRLPAYENV 335
DB 301 NTVYSTVEIPKKEHPHSLTTPDTPRLPAYENV 335
DB 301 NTVYSTVEIPKKEHPHSLTTPDTPRLPAYENV 335
```

## RESULT 2

Q9NY08 PRELIMINARY; PRT; 335 AA.

```
AC Q9NY08;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 19A protein.
GN 19A.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy J.U., Norton J.D., Hobby P., Sutton B.U.;
RT "An early response gene that encodes an immunoglobulin superfamily
RT member with structural similarity to CD2.";
RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ276429; CAB81950.2; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR SMART: SM00409; IG, 1.
DR PROSITE: PS50835; IG_LIKE; 1.
SQ SEQUENCE 335 AA; 37403 MW; BB758B505CA4DD55 CRC64;
```

Query Match 99.8%; Score 1769; DB 4; Length 335;  
Best Local Similarity 99.7%; Pred. No. 1.2e-158;  
Matches 334; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAGSPFTCLTLIYIQLTGSAAAGPVKEIVSGAVTFPLSKYKQVDSIWTNTTPTL 60
DB 1 MAGSPFTCLTLIYIQLTGSAAAGPVKEIVSGAVTFPLSKYKQVDSIWTNTTPTL 60
QY 61 VTIOPEGGTTIVTQNRNRRVDFPDGYSLSKLKSKNDGSIYVGIYSSSIQOPSTOY 120
DB 61 VTIOPEGGTTIVTQNRNRRVDFPDGYSLSKLKSKNDGSIYVGIYSSSIQOPSTOY 120
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Db      61  VTIQPEGGIIIVTONRRERVDPPDGGYSLKSLKKNDSIGIYVGIYSSSLQOPESTQEX 120
      121  VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
      121  VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
Qy      181  PISMRGSDMTFCVARNPVSRNFPSSPILARKLCEGAADDPSSWVLLCLLVPLLSL 240
      181  PISMRGSDMTFCVARNPVSRNFPSSPILARKLCEGAADDPSSWVLLCLLVPLLSL 240
Db      241  FVLGLFWMFLKRGQEEYIEKKKVDICRETPNICPSGENTEXTDITPHNRTILKEDPA 300
      241  FVLGLFWMFLKRGQEEYIEKKKVDICRETPNICPSGENTEXTDITPHNRTILKEDPA 300
Qy      301  NTVYSTVEIPKQENPHSLTMDPTPLFAVENVI 335
      301  NTVYSTVEIPKQENPHSLTMDPTPLFAVENVI 335

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## RESULT 3

```

ID      Q8ND23  PRELIMINARY;  PRT;  328 AA.
AC      Q8ND23;
DT      01-OCT-2000 (T-EMBLrel. 15, Created)
DT      01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT      01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE      19A24 protein.
GN      19A24.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RS      SEQUENCE FROM N.A.
RC      TISSUE=Peripheral blood;
RA      Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT      "An early response gene that encodes an immunoglobulin superfamily
RT      member with structural similarity to CD2."
RL      Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AJ271869; CAB76561.1; -
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      SMART; SM00409; IG_1.
DR      PROSITE; PS50835; IG_LIKE; 1.
SQ      SEQUENCE 328 AA; 36490 MW; E68A7243964380DB CRC64;

```

Query Match 78.6%; Score 1392.5; DB 4; Length 328;  
 Best Local Similarity 86.4%; Pred. No. 4.7e-123;  
 Matches 273; Conservative 3; Mismatches 5; Indels 35; Gaps 3;

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Qy      1  MAGSPFCLTIYILMQLTGSAAAGPYKELVSGVAVTFPLKSKVKQVDSIWTFTTPL 60
      1  MAGSPFCLTIYILMQLTGSAAAGPYKELVSGVAVTFPLKSKVKQVDSIWTFTTPL 60
Db      61  VTIQPEGGIIIVTONRRERVDPPDGGYSLKSLKKNDSIGIYVGIYSSSLQOPESTQEX 120
      61  VTIQPEGGIIIVTONRRERVDPPDGGYSLKSLKKNDSIGIYVGIYSSSLQOPESTQEX 120
Db      61  VTIQPEGGIIIVTONRRERVDPPDGGYSLKSLKKNDSIGIYVGIYSSSLQOPESTQEX 120
      61  VTIQPEGGIIIVTONRRERVDPPDGGYSLKSLKKNDSIGIYVGIYSSSLQOPESTQEX 120
Qy      121  VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
      121  VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
Db      121  VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
      121  VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
Qy      181  PISMRGSDMTFCVARNPVSRNFPSSPILARKLCEGAADDPSSWVLLCLLVPLLSL 240
      181  PISMRGSDMTFCVARNPVSRNFPSSPILARKLCEGAADDPSSWVLLCLLVPLLSL 240
Db      181  PISMRGSDMTFCVARNPVSRNFPSSPILARKLCEGAADDPSSWVLLCLLVPLLSL 240
      181  PISMRGSDMTFCVARNPVSRNFPSSPILARKLCEGAADDPSSWVLLCLLVPLLSL 240
Qy      241  FVLGLFWMFLKRGQEEYIEKKKVDICRETPNICPSGENTEXTDITPHNRTILKEDPA 300
      241  FVLGLFWMFLKRGQEEYIEKKKVDICRETPNICPSGENTEXTDITPHNRTILKEDPA 300
Db      241  FVLGLFWMFLKRGQEEYIEKKKVDICRETPNICPSGENTEXTDITPHNRTILKEDPA 300
      241  FVLGLFWMFLKRGQEEYIEKKKVDICRETPNICPSGENTEXTDITPHNRTILKEDPA 300
Qy      301  NTVYSTVEIPKQENPHSLTMDPTPLFAVENVI 335
      301  NTVYSTVEIPKQENPHSLTMDPTPLFAVENVI 335

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Db 269 ---YSTVEIPKQENPHSLTMDPTPLFAVENVI 335

## RESULT 4

```

ID      Q8N6Y8  PRELIMINARY;  PRT;  296 AA.
AC      Q8N6Y8;
DT      01-OCT-2002 (T-EMBLrel. 22, Created)
DT      01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE      19A24 protein.
GN      19A24.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RS      SEQUENCE FROM N.A.
RC      TISSUE=Lung;
RA      Straubeberg R.;
RL      Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
DR      EMBL; BC027867; AAH27867.1; -
DR      InterPro; IPR007110; IG-like.
DR      PROSITE; PS50835; IG_LIKE; 1.
SQ      SEQUENCE 296 AA; 32581 MW; E85D277192494EEC CRC64;

```

Query Match 76.1%; Score 1349; DB 4; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-119;  
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MAGSPFCLTIYILMQLTGSAAAGPYKELVSGVAVTFPLKSKVKQVDSIWTFTTPL 60
      1  MAGSPFCLTIYILMQLTGSAAAGPYKELVSGVAVTFPLKSKVKQVDSIWTFTTPL 60
Db      61  VTIQPEGGIIIVTONRRERVDPPDGGYSLKSLKKNDSIGIYVGIYSSSLQOPESTQEX 120
      61  VTIQPEGGIIIVTONRRERVDPPDGGYSLKSLKKNDSIGIYVGIYSSSLQOPESTQEX 120
Qy      121  VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
      121  VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
Db      121  VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
      121  VLVHYEHLSPKPYTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
Qy      181  PISMRGSDMTFCVARNPVSRNFPSSPILARKLCEGAADDPSSWVLLCLLVPLLSL 240
      181  PISMRGSDMTFCVARNPVSRNFPSSPILARKLCEGAADDPSSWVLLCLLVPLLSL 240
Db      181  PISMRGSDMTFCVARNPVSRNFPSSPILARKLCEGAADDPSSWVLLCLLVPLLSL 240
      181  PISMRGSDMTFCVARNPVSRNFPSSPILARKLCEGAADDPSSWVLLCLLVPLLSL 240
Qy      241  FVLGLFWMFLKRGQEEYIEKKKVDICRETPNICPSGENTEXTDITPHNRTILKEDPA 300
      241  FVLGLFWMFLKRGQEEYIEKKKVDICRETPNICPSGENTEXTDITPHNRTILKEDPA 300
Db      241  FVLGLFWMFLKRGQEEYIEKKKVDICRETPNICPSGENTEXTDITPHNRTILKEDPA 300
      241  FVLGLFWMFLKRGQEEYIEKKKVDICRETPNICPSGENTEXTDITPHNRTILKEDPA 300
Qy      301  NTVYSTVEIPKQENPHSLTMDPTPLFAVENVI 335
      301  NTVYSTVEIPKQENPHSLTMDPTPLFAVENVI 335

```

Query Match 65.5%; Score 1160.5; DB 4; Length 228;  
Best Local Similarity 68.1%; Pred. No. 2.4e-101;  
Matches 228; Conservative 0; Mismatches 0; Indels 107; Gaps 1;

```
QY 1 MAGSPCTCLTYILYIMQLTGSAAAGPVKEIVSGAVTPELKSRYQVDSIVWTFNTPL 60
DB 1 MAGSPCTCLTYILYIMQLTGSAAAGPVKEIVSGAVTPELKSRYQVDSIVWTFNTPL 18
QY 61 VTIQPEGGTIIYQNNRERVPDPGGYSLKSLKKKNDGIIYVGIYSSSLQGPSTGEY 120
DB 19 -----
QY 121 VLAHYEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHEGEEDVIYTWKALGOAANESHNGSIL 180
DB 19 -----EHLSPKRYTMGLQSNKNGTCVTNLTCCMEHEGEEDVIYTWKALGOAANESHNGSIL 73
QY 181 PISMRGSDMTFTICVARNPVSRNPSPTLARKLCEGAADDPDSMWLLCLLIVPLLSL 240
DB 74 PISMRGSDMTFTICVARNPVSRNPSPTLARKLCEGAADDPDSMWLLCLLIVPLLSL 133
QY 241 FVLGLFLWFLKRRQREYIEKKRVDCRETPNICPSGENTYDTIPIHTNRTILKEDPA 300
DB 134 FVLGLFLWFLKRRQREYIEKKRVDCRETPNICPSGENTYDTIPIHTNRTILKEDPA 193
QY 301 NTYVSTVEIIPKCMENPHSLTMPDTPRLFAVENVI 335
DB 194 NTYVSTVEIIPKCMENPHSLTMPDTPRLFAVENVI 228
```

RESULT 6  
Q8BHK6 PRELIMINARY; PRT; 333 AA.

```
ID 08BHK6;
AC 08BHK6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to 19A24 protein homolog.
GN 4930560D03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RC STRAIN=Morta;
RC SEQUENCE FROM N.A.
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK030135; BAC26801.1; -
DR EMBL; AK030148; BAC26810.1; -
DR EMBL; AK040678; BAC30665.1; -
DR PIR; P70566; P70566.
DR MGD; MGI:1922595; 4930560D03RIK.
DR InterPro; IPR007110; IG-1-like.
DR PROSITE; PS50835; IG-Like; 1.
SQ SEQUENCE 333 AA; 37217 MW; 0CC9A0AFAEC46E CRC64;
```

Query Match 46.1%; Score 817; DB 11; Length 333;  
Best Local Similarity 49.6%; Pred. No. 1.2e-68;  
Matches 168; Conservative 59; Mismatches 102; Indels 10; Gaps 4;

```
QY 1 MAGSPCTCLTYILYIMQLTGSAAAGPVKEIVSGAVTPELKSRYQVDSIVWTFNTPL 60
DB 1 MAFSTYIIIFTSVLCQLTYTAASGTLKVAAGLDGVSFTLNTIEIKVDYVWTFNTPL 60
QY 61 VTIQPEGGTIIYQNNRERVPDPGGYSLKSLKKKNDGIIYVGIYSSSLQGPSTGEY 120
DB 61 AMVKKDG---VTSQSNKERIVFPDGLYSMKLSQLKKNDGAVRAEIVSTSSQASLIQBY 117
```

```
QY 121 VLAHYEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHEGEEDVIYTWKALGOAANESHNGSIL 180
DB 118 VLAHYKHLSPKRVITIDRQSNKNGTCVTNLTCCSDGENTVYSKVAQGNQGFIDGATL 177
QY 181 PISMRGSDMTFTICVARNPVSRNPSPTLARKLCEGAADDPDSMWLLCLLIVPLLSL 240
DB 178 SIAMRSGEKDQALTCMARNPVSNFSPTVPFOKCEDAATLTLRGILYILCFSAVIL 237
QY 241 F--VLGLF--LWFLKRRQREYIEKKRVDCRETPNICPSGENTYDTIPIHTNRTILK 296
DB 238 FAVLLTIHTTWIKKRGKCE---EDKKRVDRQHEPDCPHLEENADVDITIPYTERKPE 294
QY 297 EDPANTVSTVEIIPKCMENPHSLTMPDTPRLFAVENVI 335
DB 295 EDPANTVSTVQIIPKVRKSPSLPAKPLVPRSLSPFENVI 333
```

RESULT 7  
Q8C64 PRELIMINARY; PRT; 335 AA.

```
ID 08C64;
AC 08C64;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Leukocyte cell-surface antigen.
DE 4930560D03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RC STRAIN=BALB/c; TISSUE=Thymus;
RC MEDLINE=2226696; PubMed=12242590;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA Bosch U., Terholet C., Engel P.;
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors."
RL Immunogenetics 54:394-402 (2002).
DR EMBL; AF467910; AAN63159.1; -
DR PIR; P70566; P70566.
DR MGD; MGI:1922595; 4930560D03RIK.
DR InterPro; IPR007110; IG-1-like.
DR PROSITE; PS50835; IG-Like; 1.
SQ SEQUENCE 335 AA; 37590 MW; 85F00ABDFC8B90A0 CRC64;
```

Query Match 43.9%; Score 778.5; DB 11; Length 335;  
Best Local Similarity 48.8%; Pred. No. 5.3e-65;  
Matches 161; Conservative 55; Mismatches 101; Indels 13; Gaps 4;

```
QY 1 MAGSPCTCLTYILYIMQLTGSAAAGPVKEIVSGAVTPELKSRYQVDSIVWTFNTPL 60
DB 1 MAFSTYIIIFTSVLCQLTYTAASGTLKVAAGLDGVSFTLNTIEIKVDYVWTFNTPL 60
QY 61 VTIQPEGGTIIYQNNRERVPDPGGYSLKSLKKKNDGIIYVGIYSSSLQGPSTGEY 120
DB 61 AMVKKDG---VTSQSNKERIVFPDGLYSMKLSQLKKNDGAVRAEIVSTSSQASLIQBY 117
QY 121 VLAHYEHLSPKRYTMGLQSNKNGTCVTNLTCCMEHEGEEDVIYTWKALGOAANESHNGSIL 180
DB 118 VLAHYKHLSPKRVITIDRQSNKNGTCVTNLTCCSDGENTVYSKVAQGNQGFIDGATL 177
QY 181 PISMRGSDMTFTICVARNPVSRNPSPTLARKLCEGAADDPDSMWLLCLLIVPLLSL 240
DB 178 SIAMRSGEKDQALTCMARNPVSNFSPTVPFOKCEDAATLTLRGILYILCFSAVIL 237
QY 241 FVLGLF-----WFLKRRQREYIEKKRVDCRETPNICPSGENTYDTIPIHTNRTILK 296
DB 238 FAVLLTIHTTWIKKRGKCE---EDKKRVDRQHEPDCPHLEENADVDITIPYTERKPE 294
QY 297 EDPANTVSTVEIIPKCMENPHSLTMPDTPRLFAVENVI 335
DB 295 EDPANTVSTVQIIPKVRKSPSLPAKPLVPRSLSPFENVI 334
```



Query Match 36.7%; Score 651; DB 11; Length 300;  
Best Local Similarity 42.4%; Pred. No. 5.1e-53;  
Matches 140; Conservative 50; Mismatches 92; Indels 48; Gaps 4;

QY 1 MAGSPCLLITLITLMOITGSAAGPYKELVSGAVTTPPLSKKQVDSIWTNTTTPPL 60  
DB 1 MARFSYIIFTSTVLCOLTVTAASGTLKVAAGALDGSVTFPLNTEIKVYVWTFNTTTPPL 60  
QY 61 VTIOPEGGTTIYTONNRREVRVDPDGYSILKSLKKNDSGIYVYGIVSSISQGPSTOXY 120  
DB 61 AMVKKDG---VTSQSNKERIVFPDGLYSKLSQLKNDSGAVRAEYISTSSQASLIQRY 117  
QY 121 VLVHVEHLSKPKVTWGLQSNKNGTCVTNLTCCEHGEEDVITYTKALQGANESHNGSIL 180  
DB 118 VLVHVKHLRSPKVTIDRQSNKNGTCVINTGCTDQDGENVTYSKMAVGQDQFHDGATL 177  
QY 181 PISMRGEGDMFTICVARNPVSNRNSPILARKLCEGAADDPDSSNVLLCLLVPLLSL 240  
DB 178 SIAMRGEKQDALTCMARNPVSNFSSTPVPQKLCEDATDLTSLRGILYILCFSAVILL 237  
QY 241 FVLGFL----WFLKREOEYIEBKRDICREFTNICHSGENIEYDTIPHTNTIILK 296  
DB 238 FAVLLTIFHTTWIKKKKKRP-----E 259  
QY 297 EDPANTVSTVEIPKEMEN---PHSILTPP 323  
DB 260 EDAPTFFYSTVQIPKVVRSQPAEHLTCQP 289

RESULT 11  
Q91XAO PRELIMINARY; PRT; 294 AA.  
AC 091XAO;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)  
DE Similar to 19A24 protein.  
GN 4930560D03RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Salivary gland;  
RA Strauberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011154; AAH1154.1; -;  
DR MGD; MGI:1922595; 4930560D03RIK.  
DR InterPro; IPR007110; IG-1like.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
SQ SEQUENCE 294 AA; 32782 MW; F4C88B04CFRA1AFB CRC64;

Query Match 36.0%; Score 637.5; DB 11; Length 294;  
Best Local Similarity 45.6%; Pred. No. 9.4e-52;  
Matches 139; Conservative 50; Mismatches 95; Indels 21; Gaps 6;

QY 1 MAGSPCLLITLITLMOITGSAAGPYKELVSGAVTTPPLSKKQVDSIWTNTTTPPL 60  
DB 1 MARFSYIIFTSTVLCOLTVTAASGTLKVAAGALDGSVTFPLNTEIKVYVWTFNTTTPPL 60  
QY 61 VTIOPEGGTTIYTONNRREVRVDPDGYSILKSLKKNDSGIYVYGIVSSISQGPSTOXY 120  
DB 61 AMVKKDG---VTSQSNKERIVFPDGLYSKLSQLKNDSGAVRAEYISTSSQASLIQRY 117  
QY 121 VLVHVEHLSKPKVTWGLQSNKNGTCVTNLTCCEHGEEDVITYTKALQGANESHNGSIL 180  
DB 118 VLVHVKHLRSPKVTIDRQSNKNGTCVINTGCTDQDGENVTYSKMAVGQDQFHDGATL 177  
QY 181 PISMRGEGDMFTICVARNPVSNRNSPILARKLCEGAADDPDSSNVLLCLLVPLLSL 240  
DB 178 SIAMRGEKQDALTCMARNPVSNFSSTPVPQKLCEDATDLTSLRGILYILCFSAVILL 237

QY 241 FVLGFL----WFLKREOEYIEBKRDICREFTN---C---PHSGENIEYDTIPHTN 291  
DB 238 FAVLLTIFHTTWIKR-----KEKTRRRRC--TKHLLFHCAQDSKESQLPACKATR 288  
QY 292 RTILK 296  
DB 289 AKVIK 293

RESULT 12  
ID 015430 PRELIMINARY; PRT; 328 AA.  
AC 015430;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)  
DE Leukocyte antigen CD84.  
GN CD84.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9745416; PubMed=9310491;  
RA De la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.;  
RT "CD84 leukocyte antigen is a new member of the Ig superfamily.";  
RL Blood 90:2398-2405 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Krause S.W., Rehl M., Heinz S., Ebner R., Andreessen R.;  
RT "Molecular cloning of MAX.3 antigen, a glycoprotein expressed on  
macrophages, platelets and megacaryocytes";  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86188202; PubMed=3008886;  
RA Andreessen R., Bros K.J., Osterholz J., Emmrich F.;  
RT "Human macrophage maturation and heterogeneity: analysis with a newly  
generated set of monoclonal antibodies to differentiation antigens";  
RL Blood 67:1257-1264 (1986).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Palou R., Sole J., Pirotto F., Gaya A.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U82988; AAB84364.1; -;  
DR EMBL; AJ223324; CAH11264.1; -;  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0006952; P:defense response; TAS.  
DR GO; GO:0007156; P:homophilic cell adhesion; TAS.  
DR InterPro; IPR003599; IG-1like.  
DR InterPro; IPR007110; IG-1like.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Signal  
SQ SEQUENCE 328 AA; 36871 MW; 6C9A89206A6D0344 CRC64;

Query Match 20.5%; Score 362.5; DB 4; Length 328;  
Best Local Similarity 31.5%; Pred. No. 1.1e-25;  
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LMQL-----TGSASGPYKELV---GSVGAVTTPPLK-SKQVDSIWTNTTTPPLVITQ 64  
DB 6 LMILLCLQITWPEAKGSEIFVTWGLIGESVTPPVNIQEBQVKIIMTSTKTSVAAYTP 65  
QY 65 PEGGT---IYTONNRREVRVDPDGYSILKSLKKNDSGIYVYGIVSSISQGPSTOXY 121  
DB 66 GDSETAIVVTVTHRYTERIALGPNYLVISDAMEDAGYKADINTQADPYTTKRYN 125  
QY 122 LVHVEHLSKPKVTWGLQSNKNGTCVTNLTCCEHGEEDVITYTKALQGANESHNGSILP 181

Db 126 LQIYRLGKPKITQSLMASVNSTCMTLTCSEVEKEKNTVWNSPLGE-----EGNVLD 179

Qy 182 ISWRMGESDMTFICVARNPVSRRFSSPIILARKLCEGAADPPDS-----SMVLLCLLVP 235

Db 180 IFQTPEDQDELTYCTAQNPNVSN--SDSISARQCADIAMGFRHTGGLSVLAMPFLVL 238

Qy 236 LLSLFLVGLFLFLFKRQREYEIEKKRVDCRETPNICPHSGENTYDTIPIHNTTL 295

Db 239 ILSSVFLFRFLF-----KRDQDAASKTITYTYIMASRNPQ--AESRIYDEILQSKVLPS 290

Qy 296 KEDPANTVSTVEIPKMEPHSLTLMPDPRLLFAVENVI 335

Db 291 KEEPVNTVSEVQFADMKGASTQDSKP--PGTSSYEIVL 328

## RESULT 13

Q8WMLP1 PRELIMINARY; PRT; 328 AA.

AC 08WMLP1

DT 01-MAR-2002 (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE CD84 antigen (leukocyte antigen).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_Taxid=9606;

RN 11

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphoma;

RA Straubeberg R.;

RU Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC020063; AA020063.1; -

DR InterPro; IPR007110; IG-like.

DR PROSITE; PS50835; IG\_LIKE; 1.

SQ SEQUENCE 328 AA; 36871 MW; 6C9A89206AD0344 CRC64;

Query Match 20.5%; Score 362.5; DB 7; Length 328;

Best Local Similarity 31.5%; Pred. No. 1.1e-25;

Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

Qy 14 LMQL-----TGSNAGPVKELV---GSVGAVTEPLK-SKYQVDSIVTNTTPTLVTIQ 64

Db 6 LMTLLCLQTPWPAAGDSEIFTVNGILGESVTFPNVIOEPQVKIIMSTKTSVAVVP 65

Qy 65 PEGGT---IIVTQNRNRERVDPPDGYSLKSLKKNDSGIYVGYSLSLQDPSTQEVY 121

Db 66 GDSPTAPVVTTHRYRERIHAGPNVNLVLSDLRMDADGADYKADINTQADPYTTKRYN 125

Qy 122 LHYHLSKPKVTMGLOSKNKGTCVNTLTCMEHGEEDVIYTKALGOANESHNSIIP 181

Db 126 LQIYRLGKPKITQSLMASVNSTCMTLTCSEVEKEKNTVWNSPLGE-----EGNVLD 179

Qy 182 ISWRMGESDMTFICVARNPVSRRFSSPIILARKLCEGAADPPDS-----SMVLLCLLVP 235

Db 180 IFQTPEDQDELTYCTAQNPNVSN--SDSISARQCADIAMGFRHTGGLSVLAMPFLVL 238

Qy 236 LLSLFLVGLFLFLFKRQREYEIEKKRVDCRETPNICPHSGENTYDTIPIHNTTL 295

Db 239 ILSSVFLFRFLF-----KRDQDAASKTITYTYIMASRNPQ--AESRIYDEILQSKVLPS 290

Qy 296 KEDPANTVSTVEIPKMEPHSLTLMPDPRLLFAVENVI 335

Db 291 KEEPVNTVSEVQFADMKGASTQDSKP--PGTSSYEIVL 328

## RESULT 14

Q92178 PRELIMINARY; PRT; 329 AA.

AC 092178

DT 01-MAY-1999 (T-EMBLrel. 10, Created)

DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE CD84 leukocyte antigen.

GN CD84.

OS Mus musculus (mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

RN 11

RP SEQUENCE FROM N.A.

RC TISSUE=Peritoneum;

RX MEDLINE=99180614; PubMed=10079287;

RA de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Boech J.,

Engel P.;

RT "Molecular cloning, characterization, and chromosomal localization of

the mouse homologue of CD84, a member of the CD2 family of cell

surface molecules.";

RL Immunogenetics 49:249-255 (1999).

DR EMBL; AF043445; AA02273.1; -

DR MGD; MGI:1336885; Cd84.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR SMART; SM00409; IG\_1.

DR PROSITE; PS50835; IG\_LIKE; 1.

SQ SEQUENCE 329 AA; 37345 MW; 43BBIASAP1989E0 CRC64;

Query Match 20.5%; Score 362.5; DB 11; Length 329;

Best Local Similarity 30.5%; Pred. No. 1.1e-25;

Matches 105; Conservative 62; Mismatches 136; Indels 41; Gaps 14;

Qy 11 IYLMQLTGSNAGPVKELV---GSVGAVTEPLK-SKYQVDSIVTNTTPTLVTIQ 65

Db 8 IYFLCLQTPWPAAGDADVPVNMNGILGESVTFILNIOEPKIDNIMWT--SQSSVAFIKPG 66

Qy 66 -BGGTIIVTQNRNRERVDPPDGYSLKSLKKNDSGIYVGYSLSLQDPSTQEVYLV 124

Db 67 VNKARVITIQGYKGRIEIIDQKYDVLVIRDLRMDADGADYKADINEN--ETIYKIYYLHI 125

Qy 125 YEHLSKPKVTMGLOSKNKGTCVNTLTCMEHGEEDVIYTKALGOANESHNSIIP 184

Db 126 YRRLKTPKTIQSLISLNTNTLTCSEVEKEKNTVWNSPLGE-----VLDIYH 179

Qy 185 RMGSDMTFICVARNPVSRRFSSPIILARKLCEGA-----ADDPSSMVLCLLVLPL 237

Db 180 SPMDQLTYTCTAQNPNV--NSDSVTVQPCPTDTPSFHRRHVLPGGLAVLFLILIPML 238

Qy 238 LSLFLVGLFLFLFKRQREYEIEKKRVDCRETP-NICPHSGENTE---YDTIPIHNT 293

Db 239 AFLFRL-----YKRRDRIVLEAD--DVSCKTVAAVSRNAQFESRIYDEIPOSKM 289

Qy 294 ILKEDPANTVSTVEIPKMEPHSLTLMPD--TPRLFAVENVI 335

Db 290 SCKDPPVTIYSSVQLSERMKTN---MKDRSLPALGNEIVV 329

## RESULT 15

Q8WML18 PRELIMINARY; PRT; 339 AA.

AC 08WML18

DT 01-MAR-2002 (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Leukocyte differentiation antigen CD84 precursor.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_Taxid=9606;

RN 11

RP SEQUENCE FROM N.A.

RA Gaya A.;

RU Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; Y12632; CAA73181.1; -

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR SMART; SM00409; IG\_1.





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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:09:07 ; Search time 54 Seconds  
(without alignments)  
1752.841 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 335

Sequence: 1 MGSPFCTLIVLMQLTGS.....PHSLTMPDRPLFAYENVY 335

Scoring table: OLIGO

Searched: 1586107 seqs, 282547505 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 700 summaries

Database:

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1: geneseq1980s:.\*  
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3: geneseq2000s:.\*  
4: geneseq2001s:.\*  
5: geneseq2002s:.\*  
6: geneseq2003as:.\*  
7: geneseq2003bs:.\*  
8: geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335	100.0	335	3 AAY66701	AAY66701 Membrane-
2	335	100.0	335	3 AAY70431	AAY70431 Human cel
3	335	100.0	335	3 AAY44609	AAY44609 Human myo
4	335	100.0	335	4 AAU29119	AAU29119 Human PRO
5	335	100.0	335	4 AAB87548	AAB87548 Human PRO
6	335	100.0	335	4 AAB47321	AAB47321 APEX-1. 8
7	335	100.0	335	4 AAB65224	AAB65224 Human PRO
8	335	100.0	335	5 AAB65873	AAB65873 Human sec
9	335	100.0	335	6 AAB58495	AAB58495 Human PRO
10	335	100.0	335	6 AABU8043	AABU8043 Novel hum
11	335	100.0	335	6 AABU84358	AABU84358 Human sec
12	335	100.0	335	6 AABR6232	AABR6232 Human sec
13	335	100.0	335	6 AABR65622	AABR65622 Human sec
14	335	100.0	335	6 AABU95562	AABU95562 Human sec
15	335	100.0	335	6 AABU58039	AABU58039 Human PRO
16	335	100.0	335	6 AABU59117	AABU59117 Novel hum
17	335	100.0	335	6 AABU82629	AABU82629 Human sec
18	335	100.0	335	6 AABU82801	AABU82801 Human PRO
19	335	100.0	335	6 AABU89922	AABU89922 Novel hum
20	335	100.0	335	6 AABR6171	AABR6171 Human sec
21	335	100.0	335	6 AABU6548	AABU6548 Human sec
22	335	100.0	335	6 AABU96224	AABU96224 Novel hum
23	335	100.0	335	6 AABU92655	AABU92655 Human sec
24	335	100.0	335	6 AABO08732	AABO08732 Human sec
25	335	100.0	335	6 AABO02784	AABO02784 Human sec

26	335	100.0	335	6 ABR74938	ABR74938 Human sec
27	335	100.0	335	6 ABR94700	ABR94700 Human sec
28	335	100.0	335	6 ABU13930	ABU13930 Human PRO
29	335	100.0	335	6 ABRU5673	ABRU5673 Human PRO
30	335	100.0	335	6 ABRU8833	ABRU8833 Novel hum
31	335	100.0	335	6 ABRU8048	ABRU8048 Novel hum
32	335	100.0	335	6 ABRU91754	ABRU91754 Novel hum
33	335	100.0	335	6 ABRU9447	ABRU9447 Human PRO
34	335	100.0	335	6 ABRU6288	ABRU6288 Human sec
35	335	100.0	335	6 ABRU7501	ABRU7501 Human sec
36	335	100.0	335	6 ABRU80529	ABRU80529 Human PRO
37	335	100.0	335	6 ABRU72515	ABRU72515 Novel hum
38	335	100.0	335	6 ABRU90898	ABRU90898 Novel hum
39	335	100.0	335	6 ABRU3957	ABRU3957 Human sec
40	335	100.0	335	6 ABRU9447	ABRU9447 Human sec
41	335	100.0	335	6 ABRU8837	ABRU8837 Human sec
42	335	100.0	335	6 ABRU16360	ABRU16360 Human sec
43	335	100.0	335	6 ABRU92260	ABRU92260 Human sec
44	335	100.0	335	6 ABRU18901	ABRU18901 Human sec
45	335	100.0	335	6 ABRU78322	ABRU78322 Human sec
46	335	100.0	335	6 ABRU1974	ABRU1974 Novel hum
47	335	100.0	335	6 ABRU5058	ABRU5058 Novel hum
48	335	100.0	335	6 ABRU00197	ABRU00197 Novel hum
49	335	100.0	335	6 ABRU11529	ABRU11529 Human sec
50	335	100.0	335	6 ABRU02174	ABRU02174 Human sec
51	335	100.0	335	6 ABRU88748	ABRU88748 Novel hum
52	335	100.0	335	6 ABRU3443	ABRU3443 Human sec
53	335	100.0	335	6 ABRU06244	ABRU06244 Novel hum
54	335	100.0	335	6 ABRU59280	ABRU59280 Human sec
55	335	100.0	335	6 ABRU09342	ABRU09342 Human sec
56	335	100.0	335	6 ABRU19206	ABRU19206 Novel hum
57	335	100.0	335	6 ABRU11224	ABRU11224 Human sec
58	335	100.0	335	6 ABRU6842	ABRU6842 Human sec
59	335	100.0	335	6 ABRU16055	ABRU16055 Human sec
60	335	100.0	335	6 ABRU13761	ABRU13761 Human sec
61	335	100.0	335	6 ABRU71528	ABRU71528 Human sec
62	335	100.0	335	6 ABRU5664	ABRU5664 Human sec
63	335	100.0	335	6 ABRU07512	ABRU07512 Human PRO
64	335	100.0	335	6 ABRU03699	ABRU03699 Human sec
65	335	100.0	335	6 ABRU67147	ABRU67147 Human sec
66	335	100.0	335	6 ABRU15750	ABRU15750 Human sec
67	335	100.0	335	6 ABRU56031	ABRU56031 Human sec
68	335	100.0	335	6 ABRU72309	ABRU72309 Human PRO
69	335	100.0	335	6 ABRU5359	ABRU5359 Human PRO
70	335	100.0	335	6 ABRU95304	ABRU95304 Novel hum
71	335	100.0	335	6 ABRU71207	ABRU71207 Human PRO
72	335	100.0	335	6 ABRU07817	ABRU07817 Human PRO
73	335	100.0	335	6 ABRU70058	ABRU70058 Human sec
74	335	100.0	335	6 ABRU69391	ABRU69391 Human sec
75	335	100.0	335	6 ABRU01532	ABRU01532 Human PRO
76	335	100.0	335	6 ABRU81334	ABRU81334 Human PRO
77	335	100.0	335	6 ABRU60131	ABRU60131 Human sec
78	335	100.0	335	6 ABRU90982	ABRU90982 Human PRO
79	335	100.0	335	6 ABRU67866	ABRU67866 Human sec
80	335	100.0	335	6 ABRU65254	ABRU65254 Human sec
81	335	100.0	335	6 ABRU68476	ABRU68476 Human sec
82	335	100.0	335	6 ABRU1888	ABRU1888 Human sec
83	335	100.0	335	6 ABRU59284	ABRU59284 Human PRO
84	335	100.0	335	6 ABRU5368	ABRU5368 Human PRO
85	335	100.0	335	6 ABRU89058	ABRU89058 Human sec
86	335	100.0	335	6 ABRU81338	ABRU81338 Human sec
87	335	100.0	335	6 ABRU4994	ABRU4994 Novel hum
88	335	100.0	335	6 ABRU0552	ABRU0552 Novel hum
89	335	100.0	335	6 ABRU4053	ABRU4053 Human sec
90	335	100.0	335	6 ABRU93704	ABRU93704 Novel hum
91	335	100.0	335	6 ABRU025961	ABRU025961 Human PRO
92	335	100.0	335	6 ABRU46499	ABRU46499 Human sec
93	335	100.0	335	6 ABRU7303	ABRU7303 Human sec
94	335	100.0	335	6 ABRU68781	ABRU68781 Human sec
95	335	100.0	335	6 ABRU06597	ABRU06597 Human sec
96	335	100.0	335	6 ABRU99142	ABRU99142 Human sec
97	335	100.0	335	6 ABRU57026	ABRU57026 Human PRO
98	335	100.0	335	6 ABRU5978	ABRU5978 Novel hum

99	335	100.0	335	6	ABU82265	Abu82265	Novel	hum	172	335	100.0	335	6	ABO44026	AbO44026	Human	PRO
100	335	100.0	335	6	ABU87276	Abu87276	Human	PRO	173	335	100.0	335	6	ADA77944	AdA77944	Human	sec
101	335	100.0	335	6	ABU83748	Abu83748	Human	sec	174	335	100.0	335	6	ABM24821	AbM24821	Human	sec
102	335	100.0	335	6	ABO08122	AbO08122	Human	PRO	175	335	100.0	335	6	ABO03089	AbO03089	Human	sec
103	335	100.0	335	6	ABU92498	Abu92498	Human	sec	176	335	100.0	335	6	ABR90345	AbR90345	Human	sec
104	335	100.0	335	6	ABU81833	Abu81833	Novel	hum	177	335	100.0	335	6	ABM17259	AbM17259	Human	sec
105	335	100.0	335	6	ABU65997	Abu65997	Novel	hum	178	335	100.0	335	6	ABR95005	AbR95005	Human	sec
106	335	100.0	335	6	ABU81168	Abu81168	Human	sec	179	335	100.0	335	6	ABR95310	AbR95310	Human	sec
107	335	100.0	335	6	ABR59826	AbR59826	Human	sec	180	335	100.0	335	6	ABR95103	AbR95103	Human	tra
108	335	100.0	335	6	ABU94014	Abu94014	Novel	hum	181	335	100.0	335	6	ABO21548	AbO21548	Human	sec
109	335	100.0	335	6	ABU99867	Abu99867	Novel	hum	182	335	100.0	335	6	ABR97812	AbR97812	Human	sec
110	335	100.0	335	6	ABR6537	AbR6537	Human	sec	183	335	100.0	335	6	ABR87600	AbR87600	Human	sec
111	335	100.0	335	6	ABR90955	AbR90955	Human	sec	184	335	100.0	335	6	ABM77641	AbM77641	Human	sec
112	335	100.0	335	6	ABO53283	AbO53283	Novel	hum	185	335	100.0	335	6	ABM27871	AbM27871	Human	sec
113	335	100.0	335	6	ABU58970	Abu58970	Human	sec	186	335	100.0	335	6	ABM06152	AbM06152	Human	sec
114	335	100.0	335	6	ABU94382	Abu94382	Human	PRO	187	335	100.0	335	6	ABM03658	AbM03658	Human	sec
115	335	100.0	335	6	ABU79254	Abu79254	Human	PRO	188	335	100.0	335	6	ABK35109	AbK35109	Human	sec
116	335	100.0	335	6	ABU86593	Abu86593	Human	sec	189	335	100.0	335	6	ABM26346	AbM26346	Human	sec
117	335	100.0	335	6	ABU86898	Abu86898	Novel	hum	190	335	100.0	335	6	ABO48128	AbO48128	Human	sec
118	335	100.0	335	6	ABU94687	Abu94687	Human	PRO	191	335	100.0	335	6	ABR92870	AbR92870	Human	sec
119	335	100.0	335	6	ABO04614	AbO04614	Human	PRO	192	335	100.0	335	6	ABO24631	AbO24631	Human	sec
120	335	100.0	335	6	ABR70363	AbR70363	Human	sec	193	335	100.0	335	6	ADA37764	AdA37764	Human	sec
121	335	100.0	335	6	ABU92248	Abu92248	Novel	hum	194	335	100.0	335	6	ABM11642	AbM11642	Human	sec
122	335	100.0	335	6	ABU98528	Abu98528	Human	PRO	195	335	100.0	335	6	ABM02743	AbM02743	Human	sec
123	335	100.0	335	6	ABR65927	AbR65927	Human	sec	196	335	100.0	335	6	ABM16039	AbM16039	Human	sec
124	335	100.0	335	6	ABR64644	AbR64644	Human	sec	197	335	100.0	335	6	ABO27600	AbO27600	Human	sec
125	335	100.0	335	6	ABU59413	Abu59413	Novel	hum	198	335	100.0	335	6	ABM29091	AbM29091	Human	sec
126	335	100.0	335	6	ABU79569	Abu79569	Human	PRO	199	335	100.0	335	6	ABM07067	AbM07067	Human	sec
127	335	100.0	335	6	ABU92960	Abu92960	Human	PRO	200	335	100.0	335	6	ABM21161	AbM21161	Human	sec
128	335	100.0	335	6	ABU95919	Abu95919	Human	sec	201	335	100.0	335	6	ABM09507	AbM09507	Human	sec
129	335	100.0	335	6	ABU91139	Abu91139	Novel	hum	202	335	100.0	335	6	ABO41377	AbO41377	Human	sec
130	335	100.0	335	6	ABU90232	Abu90232	Novel	hum	203	335	100.0	335	6	ABO36192	AbO36192	Human	PRO
131	335	100.0	335	6	ABO09647	AbO09647	Human	sec	204	335	100.0	335	6	ABO43721	AbO43721	Human	PRO
132	335	100.0	335	6	ABR58417	AbR58417	Human	NOV	205	335	100.0	335	6	ABM766421	AbM766421	Human	sec
133	335	100.0	335	6	ABO10919	AbO10919	Human	sec	206	335	100.0	335	6	ABM76117	AbM76117	Human	sec
134	335	100.0	335	6	ABR70973	AbR70973	Human	sec	207	335	100.0	335	6	ABM25736	AbM25736	Human	sec
135	335	100.0	335	6	ABU98285	Abu98285	Novel	hum	208	335	100.0	335	6	ABM26041	AbM26041	Human	sec
136	335	100.0	335	6	ABU87581	Abu87581	Human	PRO	209	335	100.0	335	6	ADA21450	AdA21450	Human	sec
137	335	100.0	335	6	ABU91449	Abu91449	Human	PRO	210	335	100.0	335	6	ABO03394	AbO03394	Human	sec
138	335	100.0	335	6	ABU899290	Abu899290	Novel	hum	211	335	100.0	335	6	ABO02479	AbO02479	Human	sec
139	335	100.0	335	6	ABU84663	Abu84663	Human	sec	212	335	100.0	335	6	ABO44261	AbO44261	Human	sec
140	335	100.0	335	6	ABR69753	AbR69753	Human	sec	213	335	100.0	335	6	ABR90650	AbR90650	Human	sec
141	335	100.0	335	6	ABU80130	Abu80130	Human	PRO	214	335	100.0	335	6	ABR73718	AbR73718	Human	sec
142	335	100.0	335	6	ABU82497	Abu82497	Novel	hum	215	335	100.0	335	6	ABO16970	AbO16970	Human	sec
143	335	100.0	335	6	ABU92179	Abu92179	Novel	hum	216	335	100.0	335	6	ABR94395	AbR94395	Human	sec
144	335	100.0	335	6	ABU93399	Abu93399	Human	PRO	217	335	100.0	335	6	ABR75902	AbR75902	Human	sec
145	335	100.0	335	6	ABO09952	AbO09952	Human	sec	218	335	100.0	335	6	ABR71278	AbR71278	Human	sec
146	335	100.0	335	6	ABO09037	AbO09037	Human	sec	219	335	100.0	335	6	ABR93175	AbR93175	Human	sec
147	335	100.0	335	6	ABU96461	Abu96461	Human	PRO	220	335	100.0	335	6	ABR93480	AbR93480	Human	sec
148	335	100.0	335	6	ABU10885	Abu10885	Human	PRO	221	335	100.0	335	6	ADA10237	AdA10237	Human	sec
149	335	100.0	335	6	ABU10605	Abu10605	Human	sec	222	335	100.0	335	6	ABR87905	AbR87905	Human	sec
150	335	100.0	335	6	ABU81637	Abu81637	Novel	hum	223	335	100.0	335	6	ABO27905	AbO27905	Human	sec
151	335	100.0	335	6	ABU72131	Abu72131	Human	PRO	224	335	100.0	335	6	ABO30040	AbO30040	Human	sec
152	335	100.0	335	6	ABU95614	Abu95614	Human	PRO	225	335	100.0	335	6	ABO33249	AbO33249	Human	PRO
153	335	100.0	335	6	ABU96883	Abu96883	Novel	hum	226	335	100.0	335	6	ABM04937	AbM04937	Human	sec
154	335	100.0	335	6	ABR70668	AbR70668	Human	sec	227	335	100.0	335	6	ABM08897	AbM08897	Human	sec
155	335	100.0	335	6	ABO05019	AbO05019	Novel	hum	228	335	100.0	335	6	ABO36497	AbO36497	Human	sec
156	335	100.0	335	6	ABO08427	AbO08427	Human	sec	229	335	100.0	335	6	ABO35582	AbO35582	Human	PRO
157	335	100.0	335	6	ABU88576	Abu88576	Human	sec	230	335	100.0	335	6	ABO39547	AbO39547	Human	sec
158	335	100.0	335	6	ABO34090	AbO34090	Human	PRO	231	335	100.0	335	6	ABM10422	AbM10422	Human	sec
159	335	100.0	335	6	ABO05634	AbO05634	Human	sec	232	335	100.0	335	6	ABM11947	AbM11947	Human	sec
160	335	100.0	335	6	ABR74023	AbR74023	Human	sec	233	335	100.0	335	6	ABO52093	AbO52093	Human	PRO
161	335	100.0	335	6	ABR95615	AbR95615	Human	sec	234	335	100.0	335	6	ABO52398	AbO52398	Human	PRO
162	335	100.0	335	6	ABR80912	AbR80912	Human	sec	235	335	100.0	335	6	ADA19908	AdA19908	Novel	hum
163	335	100.0	335	6	ABR81217	AbR81217	Human	sec	236	335	100.0	335	6	ABO23716	AbO23716	Human	sec
164	335	100.0	335	6	ABM00913	AbM00913	Human	sec	237	335	100.0	335	6	ABM17291	AbM17291	Human	tra
165	335	100.0	335	6	ABR88515	AbR88515	Human	sec	238	335	100.0	335	6	ADA17781	AdA17781	Human	PRO
166	335	100.0	335	6	ABM77336	AbM77336	Human	sec	239	335	100.0	335	6	ABR97202	AbR97202	Human	sec
167	335	100.0	335	6	ABO28820	AbO28820	Human	sec	240	335	100.0	335	6	ABR86590	AbR86590	Human	sec
168	335	100.0	335	6	ABO31565	AbO31565	Human	sec	241	335	100.0	335	6	ABM11032	AbM11032	Human	sec
169	335	100.0	335	6	ABM07982	AbM07982	Human	sec	242	335	100.0	335	6	ABM28176	AbM28176	Human	sec
170	335	100.0	335	6	ABO40462	AbO40462	Human	sec	243	335	100.0	335	6	ABO32175	AbO32175	Human	sec
171	335	100.0	335	6	ABO35887	AbO35887	Human	PRO	244	335	100.0	335	6	ABM15302	AbM15302	Human	sec

245	335	100.0	335	6	ABM06457	Abm06457	Human	sec	318	335	100.0	335	6	ABO28515	AbO28515	Human	sec
246	335	100.0	335	6	ABM04268	Abm04268	Human	sec	319	335	100.0	335	6	ABO30345	AbO30345	Human	sec
247	335	100.0	335	6	ABM22381	Abm22381	Human	sec	320	335	100.0	335	6	ABM07372	Abm07372	Human	sec
248	335	100.0	335	6	ABM07677	Abm07677	Human	sec	321	335	100.0	335	6	ABM03963	Abm03963	Human	sec
249	335	100.0	335	6	ABO40767	AbO40767	Human	sec	322	335	100.0	335	6	ABO37107	AbO37107	Human	sec
250	335	100.0	335	6	ABM35414	Abm35414	Human	sec	323	335	100.0	335	6	ABO41682	AbO41682	Human	sec
251	335	100.0	335	6	ABM33177	Abm33177	Human	sec	324	335	100.0	335	6	ABO35277	AbO35277	Human	sec
252	335	100.0	335	6	ABM32703	Abm32703	Human	PRO	325	335	100.0	335	6	ABM25126	AbM25126	Human	sec
253	335	100.0	335	6	ABO50263	AbO50263	Human	sec	326	335	100.0	335	6	ABO47518	AbO47518	Human	sec
254	335	100.0	335	6	ABU99257	Abu99257	Human	sec	327	335	100.0	335	6	ABO47823	AbO47823	Human	sec
255	335	100.0	335	6	ABO04309	AbO04309	Human	sec	328	335	100.0	335	6	ABO48433	AbO48433	Human	sec
256	335	100.0	335	6	ABO05939	AbO05939	Human	sec	329	335	100.0	335	6	ABO51483	AbO51483	Human	PRO
257	335	100.0	335	6	ABM18479	Abm18479	Human	sec	330	335	100.0	335	6	ABO51788	AbO51788	Human	PRO
258	335	100.0	335	6	ADA27889	Ada27889	Human	sec	331	335	100.0	335	6	ABO50568	AbO50568	Human	sec
259	335	100.0	335	6	ABR9507	AbR9507	Human	sec	332	335	100.0	335	6	ABR79652	AbR79652	Human	sec
260	335	100.0	335	6	ABR80607	AbR80607	Human	sec	333	335	100.0	335	6	ABM16954	Abm16954	Human	sec
261	335	100.0	335	6	ABM01218	Abm01218	Human	sec	334	335	100.0	335	6	ABO17986	AbO17986	Human	sec
262	335	100.0	335	6	ABR88820	AbR88820	Human	sec	335	335	100.0	335	6	ABO20938	AbO20938	Human	sec
263	335	100.0	335	6	ABM13472	Abm13472	Human	sec	336	335	100.0	335	6	ABR96897	AbR96897	Human	sec
264	335	100.0	335	6	ABM20856	Abm20856	Human	sec	337	335	100.0	335	6	ADA38694	Ada38694	Human	sec
265	335	100.0	335	6	ABO41987	AbO41987	Human	sec	338	335	100.0	335	6	ABM12252	Abm12252	Human	sec
266	335	100.0	335	6	ABO42597	AbO42597	Human	sec	339	335	100.0	335	6	ABM16344	Abm16344	Human	sec
267	335	100.0	335	6	ABM10117	Abm10117	Human	sec	340	335	100.0	335	6	ABM24211	Abm24211	Human	sec
268	335	100.0	335	6	ABO38632	AbO38632	Human	sec	341	335	100.0	335	6	ABM14692	Abm14692	Human	sec
269	335	100.0	335	6	ABM32872	Abm32872	Human	sec	342	335	100.0	335	6	ABM04573	Abm04573	Human	sec
270	335	100.0	335	6	ABM22686	Abm22686	Human	sec	343	335	100.0	335	6	ABM06762	Abm06762	Human	sec
271	335	100.0	335	6	ABM74897	Abm74897	Human	sec	344	335	100.0	335	6	ABM09202	Abm09202	Human	sec
272	335	100.0	335	6	ADA79736	Ada79736	Human	sec	345	335	100.0	335	6	ABO39242	AbO39242	Human	sec
273	335	100.0	335	6	ABR96287	AbR96287	Human	sec	346	335	100.0	335	6	ABM75507	Abm75507	Human	sec
274	335	100.0	335	6	ABM02438	Abm02438	Human	sec	347	335	100.0	335	6	ABM25431	Abm25431	Human	sec
275	335	100.0	335	6	ABR86380	AbR86380	Human	sec	348	335	100.0	335	6	ABM19941	Abm19941	Human	sec
276	335	100.0	335	6	ABR86685	AbR86685	Human	sec	349	335	100.0	335	6	ABO46847	AbO46847	Human	PRO
277	335	100.0	335	6	ABM16649	Abm16649	Human	sec	350	335	100.0	335	6	ABO47152	AbO47152	Human	PRO
278	335	100.0	335	6	ABM29701	Abm29701	Human	sec	351	335	100.0	335	6	ABR83261	AbR83261	Human	sec
279	335	100.0	335	6	ABO29125	AbO29125	Human	sec	352	335	100.0	335	6	ABR71583	AbR71583	Human	sec
280	335	100.0	335	6	ABM23906	Abm23906	Human	sec	353	335	100.0	335	6	ABR72193	AbR72193	Human	sec
281	335	100.0	335	6	ABM32396	Abm32396	Human	sec	354	335	100.0	335	6	ABR98532	AbR98532	Human	sec
282	335	100.0	335	6	ABM22076	Abm22076	Human	sec	355	335	100.0	335	6	ABO06902	AbO06902	Human	sec
283	335	100.0	335	6	ABO37717	AbO37717	Human	sec	356	335	100.0	335	6	ABR84855	AbR84855	Human	sec
284	335	100.0	335	6	ABM28481	Abm28481	Human	sec	357	335	100.0	335	6	ABR73413	AbR73413	Human	sec
285	335	100.0	335	6	ABM28786	Abm28786	Human	sec	358	335	100.0	335	6	ABR76507	AbR76507	Human	sec
286	335	100.0	335	6	ABM66430	Abm66430	Human	sec	359	335	100.0	335	6	ABR73108	AbR73108	Human	sec
287	335	100.0	335	6	ABM75812	Abm75812	Human	sec	360	335	100.0	335	6	ABM18174	Abm18174	Human	sec
288	335	100.0	335	6	ABM34092	Abm34092	Human	sec	361	335	100.0	335	6	ABO20633	AbO20633	Human	sec
289	335	100.0	335	6	ABM34397	Abm34397	Human	sec	362	335	100.0	335	6	ABO25376	AbO25376	Human	PRO
290	335	100.0	335	6	ABO20328	AbO20328	Human	sec	363	335	100.0	335	6	ABO25681	AbO25681	Human	PRO
291	335	100.0	335	6	ABO21243	AbO21243	Human	sec	364	335	100.0	335	6	ABR94090	AbR94090	Human	sec
292	335	100.0	335	6	ABO22158	AbO22158	Human	sec	365	335	100.0	335	6	ADA92815	Ada92815	Human	sec
293	335	100.0	335	6	ADA20080	Ada20080	Novel	hum	366	335	100.0	335	6	ABR79997	AbR79997	Human	sec
294	335	100.0	335	6	ABO34189	AbO34189	Human	sec	367	335	100.0	335	6	ABM11337	Abm11337	Human	sec
295	335	100.0	335	6	ABR96592	AbR96592	Human	sec	368	335	100.0	335	6	ABO32944	AbO32944	Human	PRO
296	335	100.0	335	6	ADA94469	Ada94469	Human	sec	369	335	100.0	335	6	ABO30650	AbO30650	Human	sec
297	335	100.0	335	6	ABR95770	AbR95770	Human	sec	370	335	100.0	335	6	ABO30955	AbO30955	Human	sec
298	335	100.0	335	6	ABR99752	AbR99752	Human	sec	371	335	100.0	335	6	ABM27261	Abm27261	Human	sec
299	335	100.0	335	6	ABM00608	Abm00608	Human	sec	372	335	100.0	335	6	ABM30006	Abm30006	Human	sec
300	335	100.0	335	6	ABM00303	Abm00303	Human	sec	373	335	100.0	335	6	ABM05542	Abm05542	Human	sec
301	335	100.0	335	6	ABO29735	AbO29735	Human	sec	374	335	100.0	335	6	ABM15607	Abm15607	Human	sec
302	335	100.0	335	6	ABM23601	Abm23601	Human	sec	375	335	100.0	335	6	ABM08592	Abm08592	Human	sec
303	335	100.0	335	6	ABM29396	Abm29396	Human	sec	376	335	100.0	335	6	ABO42292	AbO42292	Human	sec
304	335	100.0	335	6	ABO38327	AbO38327	Human	sec	377	335	100.0	335	6	ABO38022	AbO38022	Human	sec
305	335	100.0	335	6	ABO45627	AbO45627	Human	PRO	378	335	100.0	335	6	ABO45932	AbO45932	Human	PRO
306	335	100.0	335	6	ABM20551	Abm20551	Human	sec	379	335	100.0	335	6	ABM66735	Abm66735	Human	sec
307	335	100.0	335	6	ADA81463	Ada81463	Human	sec	380	335	100.0	335	6	AD820304	Ad820304	Human	sec
308	335	100.0	335	6	ABO16665	AbO16665	Human	sec	381	335	100.0	335	6	ABM19636	Abm19636	Human	sec
309	335	100.0	335	6	ABO18291	AbO18291	Human	sec	382	335	100.0	335	6	ABO49348	AbO49348	Human	sec
310	335	100.0	335	6	ABO22718	AbO22718	Human	PRO	383	335	100.0	335	6	ABO49653	AbO49653	Human	sec
311	335	100.0	335	6	ABO23023	AbO23023	Human	PRO	384	335	100.0	335	6	AD878556	Ad878556	Human	sec
312	335	100.0	335	6	ABR92565	AbR92565	Human	sec	385	335	100.0	335	6	ABR88210	AbR88210	Human	sec
313	335	100.0	335	6	ABR81522	AbR81522	Human	sec	386	335	100.0	335	6	ADA00377	Ada00377	Human	sec
314	335	100.0	335	6	ABM77946	Abm77946	Human	sec	387	335	100.0	335	6	ABM26956	Abm26956	Human	sec
315	335	100.0	335	6	ABR89735	AbR89735	Human	sec	388	335	100.0	335	6	ABM03353	Abm03353	Human	sec
316	335	100.0	335	6	ABM26651	Abm26651	Human	sec	389	335	100.0	335	6	ABO39852	AbO39852	Human	sec
317	335	100.0	335	6	ABM13777	Abm13777	Human	sec	390	335	100.0	335	7	ABO49958	AbO49958	Human	sec

391	335	100.0	335	7	ABO50873	ABO50873	Human	sec	464	335	100.0	335	7	ABW22991	Abm22991	Human	sec
392	335	100.0	335	7	ABO05329	ABO05329	Human	sec	465	335	100.0	335	7	ABW30311	Abm30311	Human	sec
393	335	100.0	335	7	ABR74633	ABr74633	Human	sec	466	335	100.0	335	7	ABW21771	Abm21771	Human	sec
394	335	100.0	335	7	ABR77112	ABr77112	Human	sec	467	335	100.0	335	7	ABW21466	Abm21466	Human	sec
395	335	100.0	335	7	ABM17869	Abm17869	Human	sec	468	335	100.0	335	7	ABM14997	Abm14997	Human	sec
396	335	100.0	335	7	ABR95920	ABr95920	Human	sec	469	335	100.0	335	7	ABO41072	ABO41072	Human	sec
397	335	100.0	335	7	ABO21853	ABO21853	Human	sec	470	335	100.0	335	7	ABO36802	ABO36802	Human	sec
398	335	100.0	335	7	ABO20023	ABO20023	Human	sec	471	335	100.0	335	7	ABO37412	ABO37412	Human	sec
399	335	100.0	335	7	ABO24336	ABO24336	Human	sec	472	335	100.0	335	7	ABW75202	ABW75202	Human	sec
400	335	100.0	335	7	ABR86075	ABr86075	Human	sec	473	335	100.0	335	7	ABM33482	Abm33482	Human	sec
401	335	100.0	335	7	ABM10727	Abm10727	Human	sec	474	335	100.0	335	7	ABO46237	ABO46237	Human	sec
402	335	100.0	335	7	ABW67766	ABw67766	Human	sec	475	335	100.0	335	7	ADB82627	ADb82627	Human	sec
403	335	100.0	335	7	ABR89430	ABr89430	Human	sec	476	335	100.0	335	7	ADB85619	ADB85619	Novel	hum
404	335	100.0	335	7	ABM12557	Abm12557	Human	sec	477	335	100.0	335	7	ADB96261	ADB96261	Human	sec
405	335	100.0	335	7	ABM05847	ABm05847	Human	sec	478	335	100.0	335	7	ABM31836	Abm31836	Human	sec
406	335	100.0	335	7	ABO34972	ABO34972	Human	sec	479	335	100.0	335	7	ABM31226	Abm31226	Human	sec
407	335	100.0	335	7	ABM03048	ABm03048	Human	PRO	480	335	100.0	335	7	ADB85935	ADB85935	Human	sec
408	335	100.0	335	7	ABM19026	ABm19026	Human	sec	481	335	100.0	335	7	ABM32141	ABM32141	Human	sec
409	335	100.0	335	7	ABM19331	ABm19331	Human	sec	482	335	100.0	335	7	ABM32446	ABM32446	Human	sec
410	335	100.0	335	7	ABO46542	ABO46542	Human	PRO	483	335	100.0	335	7	ADB68298	ADB68298	Human	PRO
411	335	100.0	335	7	ABO49043	ABO49043	Human	sec	484	335	100.0	335	7	ADB68105	ADB68105	Human	PRO
412	335	100.0	335	7	ABR69086	ABr69086	Human	sec	485	335	100.0	335	7	ABM31531	ABM31531	Human	sec
413	335	100.0	335	7	ABR89125	ABr89125	Human	sec	486	335	100.0	335	7	ABM30921	ABm30921	Human	sec
414	335	100.0	335	7	ABR72438	ABr72438	Human	sec	487	335	100.0	335	7	ADB90922	ADB90922	Novel	hum
415	335	100.0	335	7	ABR74328	ABr74328	Human	sec	488	335	100.0	335	7	ADC57733	ADC57733	Human	PRO
416	335	100.0	335	7	ABO18596	ABO18596	Human	sec	489	335	100.0	335	7	ADC55097	ADC55097	Human	PRO
417	335	100.0	335	7	ABR80302	ABr80302	Human	sec	490	335	100.0	335	7	ADC11964	ADC11964	Human	sec
418	335	100.0	335	7	ABM01523	ABm01523	Human	sec	491	335	100.0	335	7	ADC07002	ADC07002	Human	PRO
419	335	100.0	335	7	ABM02133	ABm02133	Human	sec	492	335	100.0	335	7	ADC56386	ADC56386	Human	PRO
420	335	100.0	335	7	ABR87295	ABr87295	Human	sec	493	335	100.0	335	7	ADC17181	ADC17181	Mammalian	
421	335	100.0	335	7	ABM12862	ABm12862	Human	sec	494	335	100.0	335	7	ADC07441	ADC07441	Human	sec
422	335	100.0	335	7	ABM30616	ABm30616	Human	sec	495	335	100.0	335	7	ADC11431	ADC11431	Human	sec
423	335	100.0	335	7	ABM24516	ABm24516	Human	sec	496	335	100.0	335	7	ADC14879	ADC14879	Novel	hum
424	335	100.0	335	7	ABO29430	ABO29430	Human	sec	497	335	100.0	335	7	ADC52374	ADC52374	Novel	hum
425	335	100.0	335	7	ABO31260	ABO31260	Human	sec	498	335	100.0	335	7	ADC14553	ADC14553	Novel	hum
426	335	100.0	335	7	ABM14367	ABm14367	Human	sec	499	335	100.0	335	7	ADC08085	ADC08085	Novel	hum
427	335	100.0	335	7	ABM09812	ABm09812	Human	sec	500	335	100.0	335	7	ADC81910	ADC81910	Human	PRO
428	335	100.0	335	7	ABO38937	ABO38937	Human	sec	501	335	100.0	335	7	ADD07552	ADD07552	Novel	hum
429	335	100.0	335	7	ABM34702	ABM34702	Human	sec	502	335	100.0	335	7	ADC82443	ADC82443	Human	PRO
430	335	100.0	335	7	ABO51178	ABO51178	Human	sec	503	335	100.0	335	7	ADD05655	ADD05655	Human	sec
431	335	100.0	335	7	ABO04004	ABO04004	Human	sec	504	335	100.0	335	7	ADD08623	ADD08623	Novel	hum
432	335	100.0	335	7	ABO10474	ABO10474	Human	PRO	505	335	100.0	335	7	ADD06872	ADD06872	Novel	hum
433	335	100.0	335	7	ABO53176	ABO53176	Human	sec	506	335	100.0	335	7	ADC89503	ADC89503	Human	nat
434	335	100.0	335	7	ABR77717	ABr77717	Human	sec	507	335	100.0	335	7	ADC83119	ADC83119	Human	PRO
435	335	100.0	335	7	ABR78927	ABr78927	Human	sec	508	335	100.0	335	7	ADD67525	ADD67525	Human	PRO
436	335	100.0	335	7	ABO24021	ABO24021	Human	sec	509	335	100.0	335	7	ADD55226	ADD55226	Human	LY1
437	335	100.0	335	7	ABR93785	ABr93785	Human	sec	510	335	100.0	335	7	ADD36050	ADD36050	Novel	hum
438	335	100.0	335	7	ABM01828	ABm01828	Human	sec	511	335	100.0	335	7	ADD56184	ADD56184	Human	PRO
439	335	100.0	335	7	ABM78251	ABm78251	Human	sec	512	335	100.0	335	7	ADD54622	ADD54622	Human	PRO
440	335	100.0	335	7	ABR90040	ABr90040	Human	sec	513	335	100.0	335	7	ADB26776	ADB26776	Novel	hum
441	335	100.0	335	7	ADA22376	ADA22376	Human	sec	514	335	100.0	335	7	ADB26243	ADB26243	Novel	hum
442	335	100.0	335	7	ABM27566	ABm27566	Human	sec	515	335	100.0	335	8	ADC52184	ADC52184	Novel	hum
443	335	100.0	335	7	ABM13167	ABm13167	Human	sec	516	335	100.0	335	8	ADB74329	ADB74329	Human	sec
444	335	100.0	335	7	ABO31870	ABO31870	Human	sec	517	335	100.0	335	8	ADB74941	ADB74941	Human	sec
445	335	100.0	335	7	ABM14082	ABM14082	Human	sec	518	335	100.0	336	3	AA332373	AA332373	Human	sec
446	335	100.0	335	7	ABM08287	ABm08287	Human	sec	519	312	99.1	312	3	AA444610	AA444610	hu	
447	335	100.0	335	7	ABO40157	ABO40157	Human	sec	520	257	76.7	328	5	ABB97472	ABB97472	Novel	hum
448	335	100.0	335	7	ABM74592	ABm74592	Human	sec	521	234	69.9	335	7	ADD18672	ADD18672	Human	dis
449	335	100.0	335	7	ABM33787	ABm33787	Human	sec	522	217	64.8	335	7	ABR58418	ABR58418	Human	NOV
450	335	100.0	335	7	ABM20246	ABm20246	Human	sec	523	110	32.8	110	3	AAW67811	AAW67811	Human	sec
451	335	100.0	335	7	ABO48728	ABO48728	Human	sec	524	110	32.8	110	2	AA332405	AA332405	Human	sec
452	335	100.0	335	7	ABO22546	ABO22546	Human	sec	525	110	32.8	110	6	ADA57321	ADA57321	Human	sec
453	335	100.0	335	7	ABR72803	ABr72803	Human	sec	526	110	32.8	110	6	ADA56750	ADA56750	Human	sec
454	335	100.0	335	7	ABO15445	ABO15445	Human	sec	527	110	32.8	110	6	ADA40601	ADA40601	Human	sec
455	335	100.0	335	7	ABR85160	ABr85160	Human	sec	528	110	32.8	110	6	ADA41198	ADA41198	Human	sec
456	335	100.0	335	7	ABO15140	ABO15140	Human	sec	529	97	29.0	97	3	AA600391	AA600391	Human	sec
457	335	100.0	335	7	ABO17275	ABO17275	Human	sec	530	97	29.0	98	2	AA511662	AA511662	Human	5'
458	335	100.0	335	7	ABM17564	ABM17564	Human	sec	531	92	27.5	684	4	ABG11697	ABG11697	Novel	hum
459	335	100.0	335	7	ADA06542	ADA06542	Human	sec	532	92	27.5	684	4	ABG12169	ABG12169	Novel	hum
460	335	100.0	335	7	ADA39235	ADA39235	Human	sec	533	91	27.2	91	4	AAW21122	AAW21122	Peptide	#
461	335	100.0	335	7	ABR85465	ABr85465	Human	sec	534	91	27.2	91	4	ABW43438	ABW43438	Peptide	#
462	335	100.0	335	7	ABM77031	ABm77031	Human	sec	535	91	27.2	91	4	AAW37326	AAW37326	Peptide	#
463	335	100.0	335	7	ABO28210	ABO28210	Human	sec	536	91	27.2	91	4	ABB26408	ABB26408	Protein	#

537	91	27.2	91	4	AAW77190	AAW77190 Human bon	610	8	2.4	360	6	ABO11142	ABO11142 Human sec
538	91	27.2	91	4	AAW64367	AAW64367 Human bra	611	8	2.4	360	6	ABR66760	ABR66760 Human sec
539	91	27.2	91	4	ABG58815	ABG58815 Human liv	612	8	2.4	360	6	ABO15973	ABO15973 Human sec
540	91	27.2	91	5	ABG46203	ABG46203 Human pep	613	8	2.4	360	6	ABO13679	ABO13679 Human sec
541	86	25.7	90	3	AAW32404	AAW32404 Human sec	614	8	2.4	360	6	ABO47399	ABO47399 Human sec
542	68	20.3	124	2	AAW12645	AAW12645 Human 5'	615	8	2.4	360	6	ABO65582	ABO65582 Human sec
543	33	9.9	3	2	AAW67932	AAW67932 Fragment	616	8	2.4	360	6	ABO07430	ABO07430 Human PRO
544	27	8.1	28	2	AAW67932	AAW67932 Fragment	617	8	2.4	360	6	ABO03617	ABO03617 Human sec
545	19	5.7	114	4	AAW87990	AAW87990 Human imm	618	8	2.4	360	6	ABR67065	ABR67065 Human sec
546	11	3.3	11	7	ADC89505	ADC89505 Human nat	619	8	2.4	360	6	ABO15668	ABO15668 Human sec
547	11	3.3	12	7	ADC89504	ADC89504 Human nat	620	8	2.4	360	6	ABU55949	ABU55949 Human sec
548	11	3.3	16	7	ADC89506	ADC89506 Human nat	621	8	2.4	360	6	ABU65277	ABU65277 Human PRO
549	9	2.7	66	3	AAW25088	AAW25088 Archaeidops	622	8	2.4	360	6	ABU95222	ABU95222 Novel hum
550	9	2.7	66	3	AAW351025	AAW351025 Archaeidops	623	8	2.4	360	6	ABU71125	ABU71125 Human PRO
551	9	2.7	456	3	ABG35025	ABG35025 Novel hum	624	8	2.4	360	6	ABO07735	ABO07735 Human PRO
552	8	2.4	15	2	AAW13308	AAW13308 Naturalily	625	8	2.4	360	6	ABR69976	ABR69976 Human sec
553	8	2.4	26	4	AAW74404	AAW74404 Deemoglet	626	8	2.4	360	6	ABR69309	ABR69309 Human sec
554	8	2.4	105	4	AAW80619	AAW80619 Envyironme	627	8	2.4	360	6	ABO01450	ABO01450 Human PRO
555	8	2.4	122	2	AAW37871	AAW37871 Human pro	628	8	2.4	360	6	ABU81252	ABU81252 Human PRO
556	8	2.4	172	4	AAW87244	AAW87244 Human EXM	629	8	2.4	360	6	ABR60049	ABR60049 Human sec
557	8	2.4	194	4	AAW40751	AAW40751 Human pol	630	8	2.4	360	6	ABR67784	ABR67784 Human sec
558	8	2.4	289	3	AAW3912	AAW3912 A human h	631	8	2.4	360	6	ABR65172	ABR65172 Human sec
559	8	2.4	306	6	ABU24508	ABU24508 Protein e	632	8	2.4	360	6	ABR68394	ABR68394 Human sec
560	8	2.4	310	6	ADW5489	ADW5489 Human pro	633	8	2.4	360	6	ABR71806	ABR71806 Human sec
561	8	2.4	360	2	AAW13381	AAW13381 Antino act	634	8	2.4	360	6	ABU85286	ABU85286 Human PRO
562	8	2.4	360	3	ADC78533	ADC78533 Human PRO	635	8	2.4	360	6	ABU88976	ABU88976 Human sec
563	8	2.4	360	4	AAW80249	AAW80249 Human PRO	636	8	2.4	360	6	ABU83056	ABU83056 Human sec
564	8	2.4	360	4	AAW29037	AAW29037 Human PRO	637	8	2.4	360	6	ABU94912	ABU94912 Novel hum
565	8	2.4	360	4	AAW38965	AAW38965 Human pol	638	8	2.4	360	6	ABU90460	ABU90460 Novel hum
566	8	2.4	360	6	ABU58413	ABU58413 Human PRO	639	8	2.4	360	6	ABU83971	ABU83971 Human sec
567	8	2.4	360	6	ABU71627	ABU71627 Human PRO	640	8	2.4	360	6	ABU93622	ABU93622 Novel hum
568	8	2.4	360	6	ABU87961	ABU87961 Novel hum	641	8	2.4	360	6	ABR64867	ABR64867 Human sec
569	8	2.4	360	6	ABU84276	ABU84276 Human sec	642	8	2.4	360	6	ABR68699	ABR68699 Human sec
570	8	2.4	360	6	ABR66150	ABR66150 Human sec	643	8	2.4	360	6	ABO06515	ABO06515 Human sec
571	8	2.4	360	6	ABR65540	ABR65540 Human sec	644	8	2.4	360	6	ABR99060	ABR99060 Human sec
572	8	2.4	360	6	ABU99480	ABU99480 Human sec	645	8	2.4	360	6	ABU65944	ABU65944 Human PRO
573	8	2.4	360	6	ABU82719	ABU82719 Human PRO	646	8	2.4	360	6	ABU64536	ABU64536 Human sec
574	8	2.4	360	6	ABU89840	ABU89840 Novel hum	647	8	2.4	360	6	ABU85896	ABU85896 Novel hum
575	8	2.4	360	6	ABU71482	ABU71482 Human PRO	648	8	2.4	360	6	ABU67382	ABU67382 Human sec
576	8	2.4	360	6	ABR68089	ABR68089 Human sec	649	8	2.4	360	6	ABU82183	ABU82183 Novel hum
577	8	2.4	360	6	ABU96142	ABU96142 Novel hum	650	8	2.4	360	6	ABU87194	ABU87194 Human PRO
578	8	2.4	360	6	ABU92573	ABU92573 Human sec	651	8	2.4	360	6	ABU83666	ABU83666 Human sec
579	8	2.4	360	6	ABO08650	ABO08650 Human sec	652	8	2.4	360	6	ABO08040	ABO08040 Human PRO
580	8	2.4	360	6	ABO02702	ABO02702 Human sec	653	8	2.4	360	6	ABO14902	ABO14902 Human sec
581	8	2.4	360	6	ABR74856	ABR74856 Human sec	654	8	2.4	360	6	ABU81751	ABU81751 Novel hum
582	8	2.4	360	6	ABR94618	ABR94618 Human sec	655	8	2.4	360	6	ABU65915	ABU65915 Human sec
583	8	2.4	360	6	ABU85591	ABU85591 Human PRO	656	8	2.4	360	6	ABR59744	ABR59744 Human sec
584	8	2.4	360	6	ABU98751	ABU98751 Novel hum	657	8	2.4	360	6	ABU93932	ABU93932 Novel hum
585	8	2.4	360	6	ABU97966	ABU97966 Novel hum	658	8	2.4	360	6	ABU99785	ABU99785 Human sec
586	8	2.4	360	6	ABU91672	ABU91672 Novel hum	659	8	2.4	360	6	ABR66455	ABR66455 Human sec
587	8	2.4	360	6	ABU71928	ABU71928 Human sec	660	8	2.4	360	6	ABR90873	ABR90873 Human sec
588	8	2.4	360	6	ABU89365	ABU89365 Human PRO	661	8	2.4	360	6	ABU94300	ABU94300 Human PRO
589	8	2.4	360	6	ABU86206	ABU86206 Human sec	662	8	2.4	360	6	ABU79182	ABU79182 Human PRO
590	8	2.4	360	6	ABU67419	ABU67419 Human sec	663	8	2.4	360	6	ABU86511	ABU86511 Human sec
591	8	2.4	360	6	ABU80447	ABU80447 Human PRO	664	8	2.4	360	6	ABU86816	ABU86816 Novel hum
592	8	2.4	360	6	ABO01811	ABO01811 Novel hum	665	8	2.4	360	6	ABU94605	ABU94605 Human PRO
593	8	2.4	360	6	ABR99365	ABR99365 Human sec	666	8	2.4	360	6	ABO04532	ABO04532 Human PRO
594	8	2.4	360	6	ABR98755	ABR98755 Human sec	667	8	2.4	360	6	ABR70281	ABR70281 Human sec
595	8	2.4	360	6	ABO16278	ABO16278 Human sec	668	8	2.4	360	6	ABU98446	ABU98446 Human PRO
596	8	2.4	360	6	ABR92178	ABR92178 Human sec	669	8	2.4	360	6	ABR65845	ABR65845 Human sec
597	8	2.4	360	6	ABO18819	ABO18819 Human sec	670	8	2.4	360	6	ABR64562	ABR64562 Human sec
598	8	2.4	360	6	ABR78240	ABR78240 Human sec	671	8	2.4	360	6	ABU79487	ABU79487 Human PRO
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600	8	2.4	360	6	ABO00115	ABO00115 Novel hum	673	8	2.4	360	6	ABU95837	ABU95837 Human PRO
601	8	2.4	360	6	ABO11447	ABO11447 Human sec	674	8	2.4	360	6	ABU91057	ABU91057 Human PRO
602	8	2.4	360	6	ABO02092	ABO02092 Human sec	675	8	2.4	360	6	ABU90150	ABU90150 Novel hum
603	8	2.4	360	6	ABU54384	ABU54384 Human sec	676	8	2.4	360	6	ABO09565	ABO09565 Human sec
604	8	2.4	360	6	ABU88666	ABU88666 Novel hum	677	8	2.4	360	6	ABO10837	ABO10837 Human sec
605	8	2.4	360	6	ABU93361	ABU93361 Human sec	678	8	2.4	360	6	ABR70891	ABR70891 Human sec
606	8	2.4	360	6	ABO06162	ABO06162 Novel hum	679	8	2.4	360	6	ABU87499	ABU87499 Human PRO
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608	8	2.4	360	6	ABO09260	ABO09260 Human sec	681	8	2.4	360	6	ABU84581	ABU84581 Human sec
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688	8	2.4	360	6	ABU10523	Human	sec
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690	8	2.4	360	6	ABU96741	Novel	hum
691	8	2.4	360	6	ABR70586	Human	sec
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694	8	2.4	360	6	ABO14841	Human	sec
695	8	2.4	360	6	ABO05552	Human	sec
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## ALIGNMENTS

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ID      AAy66701 standard; protein; 335 AA.
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AC      AAy66701;
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DT      05-APR-2000 (first entry)
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DE      Membrane-bound protein PRO1138.
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KW      Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KM      pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS      Homo sapiens.
XX
PN      WO963088-A2.
XX
PD      09-DEC-1999.
XX
PF      02-JUN-1999; 99WO-US012252.
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 PR 16-SEP-1998; 98US-0100634P.  
 PR 12-JAN-1999; 99US-0115565P.

XX (GENTH ) GENENTECH INC.

PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;

DR WPI; 2000-072883/06.  
 DR N-PSDB; AAZ65040.

XX Membrane-bound proteins and related nucleotide sequences.

PT Claim 12; Fig 171; 822bp; English.

XX The invention provides membrane-bound PRO polypeptides and  
 PS polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIB  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
 CC also be useful for the preparation of PRO polypeptides, especially by  
 CC recombinant techniques

XX Sequence 335 AA;

Query Match 100.0%; Score 335; DB 3; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-314;  
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MAAAPTCLTLLIYIMOLTSAAAGPVELGVSGAGTFFPKSKVKQVDSIWTENTPL 60  
 QY 61 VTIQPEGGTIIIVQNNRERVDPPDGYSLKSLKKNDGIVYVGIYSSSLQGPSTQEX 120

DB 61 VTIQPEGGTIIIVQNNRERVDPPDGYSLKSLKKNDGIVYVGIYSSSLQGPSTQEX 120  
 QY 121 VLAHYHLKSKPTTWMGLQSNKCTCVTNLTTCHEHEBEDYIYWKALGQANSHNGSIL 180  
 DB 121 VLAHYHLKSKPTTWMGLQSNKCTCVTNLTTCHEHEBEDYIYWKALGQANSHNGSIL 180  
 QY 181 PISMRGSDMPTICVARNPVSNRSPILARLTCGAADDPSSNVLTCLLVPLLSL 240  
 DB 181 PISMRGSDMPTICVARNPVSNRSPILARLTCGAADDPSSNVLTCLLVPLLSL 240  
 QY 241 FVLGLFLMFLKRRQREYIEKKRVDICRETPNICPHSGENTBYDTIPHTNRTILKEDPA 300  
 DB 241 FVLGLFLMFLKRRQREYIEKKRVDICRETPNICPHSGENTBYDTIPHTNRTILKEDPA 300  
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 DB 301 NTYSTEVEIPKKNENPHSLTTPMDTPRLPAYENV 335

# RESULT 2

ID AAY70431 standard; protein; 335 AA.

XX AAY70431;

DT 21-JUN-2000 (first entry)

XX Human cell surface immunomodulator-1 (CSIMM-1).

KM Cell surface immunomodulator-1; CSIMM-1; cell proliferation; CD84;  
 KM differentiation; signal transduction; drug screening; prevention;  
 KM treatment; cancer; leukaemia; melanoma; immune disorder; AIDS;  
 KM rheumatoid arthritis; ascites; atherosclerosis; diabetes mellitus;  
 KM emphysema; irritable bowel syndrome; multiple sclerosis; diagnosis;  
 KM osteoporosis; psoriasis; microbial infections; cytotoxic; antiarthritic;  
 KM antidiabetic; immunosuppressive; antiarteriosclerotic; anti-HIV;  
 KM antiinflammatory; neuroprotective; osteopathic;  
 KM antiproliferative; antimicrobial; human.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..22 /label= Signal\_peptide

FT Protein 23..335 /label= Mature\_CSIMM-1

FT Region 34..107 /note= "Homologous to immunoglobulin domain"

FT Modified-site 89 /note= "Potential Protein kinase C phosphorylation site"

FT Modified-site 98 /note= "Potential N-glycosylation site"

FT Modified-site 103 /note= "Potential tyrosine kinase phosphorylation site"

FT Modified-site 116 /note= "Potential Casein kinase II phosphorylation site"

FT Modified-site 139 /note= "Potential Protein kinase C phosphorylation site"

FT Modified-site 142 /note= "Potential N-glycosylation site"

FT Modified-site 148 /note= "Potential N-glycosylation site"

FT Modified-site 163 /note= "Potential Protein kinase C phosphorylation site"

FT Modified-site 172 /note= "Potential N-glycosylation site"

FT Modified-site 176 /note= "Potential N-glycosylation site"

FT Modified-site 183 /note= "Potential Protein kinase C phosphorylation site"

FT Modified-site 204 /note= "Potential N-glycosylation site"

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QY	121	VLAHYEHLSPKPYTMGLQSNKNGTCVTNLTCMEHGEBDVIYTKALGQANESHNGSIL	180	
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QY	241	FLVGLFLMFLKREOREEYIEEKRRVDICRETPNICPHSGENTERYDTPHTNRTILKEDPA	300
DB	241	FLVGLFLMFLKREOREEYIEEKRRVDICRETPNICPHSGENTERYDTPHTNRTILKEDPA	300
QY	301	NTVYSTEVEIPKKMENPHSLITMPDTPRLPAYENVNI	335
DB	301	NTVYSTEVEIPKKMENPHSLITMPDTPRLPAYENVNI	335
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AAAY44609	AAAY44609 standard; protein; 335 AA.		
AC	AAAY44609;		
DT	07-APR-2000 (first entry)		
DE	Human myocardium protein-7.		
KM	Human myocardium protein-7; MP-7; congestive heart failure;		
KW	cardiovascular disorder; cardiomyopathy; hypertension; atherosclerosis;		
KW	coronary artery spasm; coronary artery disease; cell-cell interaction;		
KM	hypotensive; cardiac; screening assay.		
OS	Homo sapiens.		
XX			
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PN	WO967387-A2.		
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PD	29-DIC-1999.		
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PF	24-JUN-1999; 99WO-US014307.		
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PR	25-JUN-1998; 98US-0090579P.		
PR	29-SEP-1998; 98US-00163284.		
PR	02-MAR-1999; 99US-00261759.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Khodadoust M;		
XX			
DR	WPI; 2000-136984/12.		
DR	N-PESDB; AAZ49571.		
XX			
PT	Novel myocardium protein-7 polynucleotides, used to modulate a variety of		
PT	cellular processes.		
XX			
PS	Claim 2; Fig 2; 116pp; English.		
CC	The present sequence is myocardium protein-7 (MP-7). MP-7 is used to		
CC	modulate a variety of cellular processes e.g. modulating the activity of		
CC	proteins involved in cardiovascular disorders like congestive heart		
CC	failure or cardiomyopathy. Diseases which can be treated include		
CC	hypertension, atherosclerosis, coronary artery spasm, and coronary artery		



CC disease. MP-7 proteins may also be used for cellular regulation of immune  
 CC cell types, cell cycle, differentiation of multipotent cells, and  
 CC modulation of cell-cell interactions. MP-7 may also be used in screening  
 CC assays to identify agonists and antagonists and to raise antibodies  
 XX

PR 30-MAR-2000; 2000MO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194467P.  
 PR 11-APR-2000; 2000US-0195975P.  
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 PR 25-APR-2000; 2000US-0199654P.  
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 DB 121 VLHVYHLSPKVTMGOSKNGCTVNTLCCMEHGEEDVITYWKALGOANESHNGSIL 180  
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 DB 181 PISRWGESDMTFICVARNPVSRRFSSPIILARKLCEGAADDPDSMTLCLLVLPLLSL 240  
 QY 241 FVLGLFLMPLKREOREYIEBKRVDCRETPTNICPSGENTEXDTIPTHNTTLKEDPA 300  
 DB 241 FVLGLFLMPLKREOREYIEBKRVDCRETPTNICPSGENTEXDTIPTHNTTLKEDPA 300  
 QY 301 NTVYSTVEIPKKNENPHSLTMDPTPLFAVENVI 335  
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 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000MO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 01-DEC-2000; 2000MO-US032678.  
 PR 20-DEC-2000; 2000MO-US034956.

RESULT 4  
 AAU29119  
 ID AAU29119 standard; protein: 335 AA.

PR 30-MAR-2000; 2000MO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194467P.  
 PR 11-APR-2000; 2000US-0195975P.  
 PR 11-APR-2000; 2000US-0196000P.  
 PR 11-APR-2000; 2000US-0196187P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-01966820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199654P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000MO-US013705.  
 PR 22-MAY-2000; 2000MO-US014042.  
 PR 30-MAY-2000; 2000MO-US014941.  
 PR 02-JUN-2000; 2000MO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000MO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 01-DEC-2000; 2000MO-US032678.  
 PR 20-DEC-2000; 2000MO-US034956.

XX AAU29119;  
 XX 18-DEC-2001 (first entry)  
 DE Human PRO polypeptide sequence #96.  
 XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KM dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KM blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KM adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 XX Homo sapiens.  
 XX MO200168848-A2.  
 XX 20-SEP-2001.  
 XX 28-FEB-2001; 2001MO-US006520.

PR 30-MAR-2000; 2000MO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194467P.  
 PR 11-APR-2000; 2000US-0195975P.  
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 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
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 PR 17-MAY-2000; 2000MO-US013705.  
 PR 22-MAY-2000; 2000MO-US014042.  
 PR 30-MAY-2000; 2000MO-US014941.  
 PR 02-JUN-2000; 2000MO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000MO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 01-DEC-2000; 2000MO-US032678.  
 PR 20-DEC-2000; 2000MO-US034956.

XX 01-MAR-2000; 2000MO-US005601.  
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 PR 14-MAR-2000; 2000US-0189320P.  
 PR 14-MAR-2000; 2000US-0189328P.  
 PR 15-MAR-2000; 2000MO-US006884.  
 PR 21-MAR-2000; 2000US-0190828P.  
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 PR 21-MAR-2000; 2000US-0191048P.  
 PR 21-MAR-2000; 2000US-0191314P.  
 PR 28-MAR-2000; 2000US-0192655P.  
 PR 29-MAR-2000; 2000US-0193032P.  
 PR 29-MAR-2000; 2000US-0193053P.

PR 30-MAR-2000; 2000MO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194467P.  
 PR 11-APR-2000; 2000US-0195975P.  
 PR 11-APR-2000; 2000US-0196000P.  
 PR 11-APR-2000; 2000US-0196187P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-01966820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0199397P.  
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 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000MO-US013705.  
 PR 22-MAY-2000; 2000MO-US014042.  
 PR 30-MAY-2000; 2000MO-US014941.  
 PR 02-JUN-2000; 2000MO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000MO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 01-DEC-2000; 2000MO-US032678.  
 PR 20-DEC-2000; 2000MO-US034956.

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Db      181 PISMRWGESDMFTICVARNPVSRNFSPIIARLCEGAADDPDSSMVLCLLVPLLSL 240
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Db      241 FVLGLFLWFLKRREROEYIEKKRVDICRETPNICPHSGENTYDTIPIHTNRTIILKEDPA 300
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Db      301 NTVYSTVEIPKKMENPHSLTTPDTPRLPAYENVI 335

RESULT 5
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ID      AAB87548 standard; protein; 335 AA.
AC      AAB87548;
XX      15-MAY-2001 (first entry)
DT      Human PRO1138.
DE      Human PRO1138.
XX      Human; PRO protein; mapping.
XX      Homo sapiens.
XX      MO200116318-A2.
XX      08-MAR-2001.
XX      24-AUG-2000; 2000MO-US023328.
PF      01-SEP-1999; 99WO-US020111.
XX      15-SEP-1999; 99WO-US0201090.
PR      07-DEC-1999; 99US-0169495P.
PR      09-DEC-1999; 99US-0170262P.
PR      11-JAN-2000; 2000US-0175481P.
PR      18-FEB-2000; 2000MO-US004341.
PR      18-FEB-2000; 2000MO-US004342.
PR      22-FEB-2000; 2000MO-US004414.
PR      01-MAR-2000; 2000MO-US005601.
PR      03-MAR-2000; 2000US-0187202P.
PR      21-MAR-2000; 2000US-0191007P.
PR      30-MAR-2000; 2000MO-US008439.
PR      25-APR-2000; 2000US-0199397P.
PR      22-MAY-2000; 2000MO-US014042.
PR      05-JUN-2000; 2000US-0209832P.
XX      (GETH ) GENENTECH INC.
XX      PA
XX      PI      Eaton DL, Filvarcoff E, Gerritsen ME, Goddard A, Godowski PJ;
XX      PI      Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX      DR      MPI; 2001-183260/18.
XX      DR      N-PSDB; AAF92080.
XX      PT      Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
XX      PT      biology, including use as hybridization probes, and in chromosome and
XX      PT      gene mapping.
XX      PS      Claim 12; Fig 46; 278bp; English.
XX      CC      The present sequence is a human PRO polypeptide (secreted and
XX      CC      transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
XX      CC      anti-PRO antibodies are useful for preparation of a medicament useful in
XX      CC      the treatment of a condition which is responsive to the PRO protein.
XX      CC      agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
XX      CC      employed as molecular weight markers for protein electrophoresis. The PRO
XX      CC      coding sequence has applications in molecular biology, including use as
XX      CC      hybridisation probes, and in chromosome and gene mapping

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XX      SQ      Sequence 335 AA;
XX      Query Match      100.0%; Score 335; DB 4; Length 335;
XX      Best Local Similarity 100.0%; Pred. No. 1.6e-314;
XX      Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MAGSPCTCLTIYIIMQLTGSAAAGPVKELVSGAVTFPLSKKYKQVDSIVMTENTPL 60
QY      61 VTIOPEGGTIIYTONRNRERVDPPDGYSLSKLSKLNKDSGTYGYGYSSTIQPSTOXY 120
Db      61 VTIOPEGGTIIYTONRNRERVDPPDGYSLSKLSKLNKDSGTYGYGYSSTIQPSTOXY 120
QY      121 VLAHYEHLSPKRVMTGLQSNKNGTCVTNLTCCMEHGEEDVITYTKALQQAANESHNGSIL 180
Db      121 VLAHYEHLSPKRVMTGLQSNKNGTCVTNLTCCMEHGEEDVITYTKALQQAANESHNGSIL 180
QY      181 PISMRWGESDMFTICVARNPVSRNFSPIIARLCEGAADDPDSSMVLCLLVPLLSL 240
Db      181 PISMRWGESDMFTICVARNPVSRNFSPIIARLCEGAADDPDSSMVLCLLVPLLSL 240
QY      241 FVLGLFLWFLKRREROEYIEKKRVDICRETPNICPHSGENTYDTIPIHTNRTIILKEDPA 300
Db      241 FVLGLFLWFLKRREROEYIEKKRVDICRETPNICPHSGENTYDTIPIHTNRTIILKEDPA 300
QY      301 NTVYSTVEIPKKMENPHSLTTPDTPRLPAYENVI 335
Db      301 NTVYSTVEIPKKMENPHSLTTPDTPRLPAYENVI 335

RESULT 6
AAB47321
ID      AAB47321 standard; protein; 335 AA.
AC      AAB47321;
XX      29-AUG-2001 (first entry)
DT      APEX-1.
DE      Antigen presenting cell expression protein; APEX-1; APEX-2; APEX-3;
XX      KW      extracellular domain; immunoglobulin-like domain; Ig-like structure;
XX      KW      N-glycosylation site; transmembrane domain; cytoplasmic domain;
XX      KW      SH2-binding motif; asthma; arteriosclerosis; AIDS; cirrhosis;
XX      KW      Crohn's disease; atopic dermatitis; autoimmune anaemia; bursitis;
XX      KW      cholecystitis; diabetes mellitus; emphysema; atrophic gastritis;
XX      KW      inflammatory bowel disease; multiple sclerosis; myasthenia gravis;
XX      KW      myocardial inflammation; pericardial inflammation; osteoarthritis;
XX      KW      osteoporosis; psoriasis; Reiter's syndrome; rheumatoid arthritis;
XX      KW      inflammation; cancer; autoimmune disease; graft rejection;
XX      KW      graft versus host disease; systemic lupus erythematosus.
XX      OS      Homo sapiens.
XX      FH      Key      Location/Qualifiers
XX      FH      Peptide      1..22
XX      FT      Protein      /label= Signal peptide
XX      FT      Domain      /label= Mature APEX-1
XX      PN      MO200146260-A2.
XX      PD      28-JUN-2001.
XX      PF      22-DEC-2000; 2000MO-US034963.
XX      PR      23-DEC-1999; 99US-0172025P.
XX      PA      (BRIM ) BRISTOL-MYERS SQUIBB CO.

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**SQ** Sequence 335 AA;

Qy 1 MAGSTCLTIIYILMOLTSASAGPEVKELVGSVGGAVTPEPLKSKTKKQVDSIVMTFNTTPL 60

Db 1 MAGSTCLTIIYILMOLTSASAGPEVKELVGSVGGAVTPEPLKSKTKKQVDSIVMTFNTTPL 60

61 VTIOEGGTIIVTQNNRERVDFPDGGYSLKSLKKNDSGIYVGIISSSLQDPSTQY 120

Db 61 VTIQEGGTIIVTQNNRRERVDPPGGYSLKLSKKKNDSGIYVVGIVSSSLQDPSTQY 120

QY 121 VLVHYEHSKPKYTMGLQSNKNGTCVTNLTCCMEHGEBDVIYTKALGOAAHESHNGSIL 180

DB 121 VLVHYEHSKPKYTMGLQSNKNGTCVTNLTCCMEHGEBDVIYTKALGOAAHESHNGSIL 180

QY 161 PISNRWGESDMTFICVARNPVSRRNESSPILARKLCEGAADPDGSMVLCTLLVPLLSJ. 240

Db 181 PISMRWGSSDMTFICVARNFVSRNFSSPILARKLCSGAADDPDSSNMTLLCLLVLPLHL 240

QY 241 EVLGLFPMFLKREOEYYIEKKRDVICRETPNI CHSGENGEYDTPHTNRILIKEDPA 300

QY 301 NTVYSTVEI PKMENPHSLTTPDTPLFAVENVI 335

Db 301 NTVYSTVEIPKKMENPHSLTMPDITPRLFAVENVI 335

## RESULT 9

### ARUTS8495

ID	ABUS8495	standard; protein; 335 AA.
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AC AB0584951

PF 21-JUN-2002; 2002US-00176492

PR	18-SEP-1997	97US-0059263P
PR	18-SEP-1997	97US-0059266P

PR 21-OCT-1997; 97US-0063486P

PR 28-OCT-1997; 97US-0063540P

PR	28-OCT-1997;	97US-0063544P
DP	28-OCT-1997;	97IS-0063564P

PR 31-OCT-1997; 97US-0063870P

PR	13-NOV-1997;	97US-0065311F
PR	21-NOV-1997;	97US-0066120P

PR	24-NOV-1997;	97US-0066772P
PR	11 DEC 1997	07115 006033ED

PR 17-DEC-1997; 97US-0069870P

PR	11-MAR-1998:	98US-0077632P
PR	10-MAR-1998:	98US-0011450P

PR 20-MAR-1998; 98US-0078886P

PR 27-MAR-1998; 98US-0079786P

PR	31-MAR-1998;	98US-0080194P.
DP	01-APR-1998;	98US-0080327P.

PR 08-APR-1998; 98US-0081049P.

PR	09-APR-1998;	98US-0081195P
PR	15-APR-1998;	98US-0081838P

PR 21-APR-1998; 98US-0082569P.

PR 28-APR-1998; 98US-0083322P

PR	29-APR-1998;	98US-0083496P.
PR	29-APR-1998;	98US-0083499P.

PR 05-MAY-1998; 98US-0084366P

PR	07-MAY-1998;	98US-0084640P
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PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.

PR 15-MAY-1998; 98US-0085700P

PK 44-MAY-1998; 98US-008639ZP

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PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103442P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MAGSPCTCLTYITLQOLGSAASGPVKELVSGAVTFPLSKSKKOYDSIWFNTPL 60
DB 1 MAGSPCTCLTYITLQOLGSAASGPVKELVSGAVTFPLSKSKKOYDSIWFNTPL 60

QY 61 VTIOPEGGIIIVTONRNERVDFFPDGYSLSKLKSKKNDSGIYYVGISSLSQPSIOEY 120
61 VTIOPEGGIIIVTONRNERVDFFPDGYSLSKLKSKKNDSGIYYVGISSLSQPSIOEY 120
DB 61 VTIOPEGGIIIVTONRNERVDFFPDGYSLSKLKSKKNDSGIYYVGISSLSQPSIOEY 120

QY 121 VLAHYEHLSPKPYTMGLQSNKNGTCVNLTCMEHGEEDVIYTWALQOANESHSNLSL 180
121 VLAHYEHLSPKPYTMGLQSNKNGTCVNLTCMEHGEEDVIYTWALQOANESHSNLSL 180
DB 121 VLAHYEHLSPKPYTMGLQSNKNGTCVNLTCMEHGEEDVIYTWALQOANESHSNLSL 180

QY 181 PLSMRGSDMTFFICVARNPVSRNPSPIILARKLCEGAADPDSSMWLLCLLVLPLLSL 240
181 PLSMRGSDMTFFICVARNPVSRNPSPIILARKLCEGAADPDSSMWLLCLLVLPLLSL 240
DB 181 PLSMRGSDMTFFICVARNPVSRNPSPIILARKLCEGAADPDSSMWLLCLLVLPLLSL 240

QY 241 FVLGLFLFWLKRROEYIEKKRVDICRETPNICPHSGENTEXTDITPHNTTILKEDPA 300
241 FVLGLFLFWLKRROEYIEKKRVDICRETPNICPHSGENTEXTDITPHNTTILKEDPA 300
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Db 241 FVLGLFLMLKGRROSEYIEBKGRVDICRETPNICHSGSNTYDITPHNRIILKEDPA 300  
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Db 301 NTYVSTVEIIPKMKENPHSLLTMPDTPRLPAYENVI 335  
RESULT 10  
ABU88043  
XX ABU88043 standard; protein; 335 AA.  
AC ABU88043;  
XX 07-JUL-2003 (first entry)  
XX  
XX Novel human secreted and transmembrane protein PRO1138.  
XX  
XX Human; secreted and transmembrane protein; PRO; gene therapy;  
KW tumour necrosis factor-alpha release; TNF-alpha release; tumour;  
KW chondrocyte proliferation; chondrocyte differentiation; tumour;  
KW adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
OS Homo sapiens.  
XX  
XX US2003032127-A1.  
XX  
XX 13-FEB-2003.  
XX  
XX 26-JUN-2002; 2002US-00183012.  
XX  
XX 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059263P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
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PR	10-SEP-1998;	98US-0099754P.
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PR	23-SEP-1998;	98US-0101475P.
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PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.

Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1,6e-314;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAGSTCTLTLYITLQNTSASGPKELVSGAVTFPLSKYKQVDSIWTNTTPTL 60

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Qy	121	VLAHYEHLSKPYMTMGLOSNNGTCVTNLTCOMEHGEEDVITYTMAALQANESHNSIL 180
Db	121	VLAHYEHLSKPYMTMGLOSNNGTCVTNLTCOMEHGEEDVITYTMAALQANESHNSIL 180
Qy	181	PISMRGSDMTFFICVARNPVSRNFSPIRLAKLCEGAADDPDSSMVLCLLVLPLLSL 240
Db	181	PISMRGSDMTFFICVARNPVSRNFSPIRLAKLCEGAADDPDSSMVLCLLVLPLLSL 240
Qy	241	FVLGLFPLPKRQEEYIEEKQVDCRETPTNICPHSGENTYDTIPIHRTTIKEDPA 300
Db	241	FVLGLFPLPKRQEEYIEEKQVDCRETPTNICPHSGENTYDTIPIHRTTIKEDPA 300
Qy	301	NTVYSTVEIPKKMENPHSLTMPDPRFAVENVI 335
Db	301	NTVYSTVEIPKKMENPHSLTMPDPRFAVENVI 335

RESULT 11

ABU84358 standard; protein, 335 AA.

ABU84358;

02-AUG-2003 (first entry)

Human secreted/transmembrane protein (PRO) #96.

Human; secreted and transmembrane protein; PRO; TNF-alpha;

tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;

tissue typing.

OS Homo sapiens.

PN US2003032112-A1.

PD 13-FEB-2003.

XX 21-JUN-2002; 2002US-00176756.

XX 18-SEP-1997; 97US-0059263P.

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XX 17-OCT-1997; 97US-0062250P.

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PR 01-OCT-1998; 98US-0102687P.

PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
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Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.6e-314;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 VTIOPEGGTIIIVTONNRRERVDPPDGYSGLKSLKLNDSGIYVYGVSSIQOPESTQRY 120  
QY 121 VLAHYEHLSPKVTWMLQSNKNGTCYTNITCCMEHGEEDVIYTWKALQGANESHNGSIL 180  
DB 121 VLAHYEHLSPKVTWMLQSNKNGTCYTNITCCMEHGEEDVIYTWKALQGANESHNGSIL 180  
QY 181 PLSMWRGESDMTFICVARNPVSRNFPSSPLARKLCGADDDPSSMWLCLLVLPLLSL 240  
DB 181 PLSMWRGESDMTFICVARNPVSRNFPSSPLARKLCGADDDPSSMWLCLLVLPLLSL 240  
QY 241 FVLGLFLWFLKREOREYIEKKRVDICRETENICPHSGENTEYDTIPTNRTILKEDPA 300  
DB 241 FVLGLFLWFLKREOREYIEKKRVDICRETENICPHSGENTEYDTIPTNRTILKEDPA 300  
QY 301 NTNVSTVEIPKKNENPHSLTMPDTPRLPAYENVI 335  
DB 301 NTNVSTVEIPKKNENPHSLTMPDTPRLPAYENVI 335

## RESULT 12

ID ABR66232 standard; protein; 335 AA.

XX ABR66232;

DT 05-AUG-2003 (first entry)

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

XX Human; PRO; secreted protein; transmembrane protein; TNF-alpha;  
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnerary; gene therapy.

XX Homo sapiens.

XX US2003027278-A1.

XX 06-FEB-2003.

PD 21-JUN-2002; 2002US-00176987.

PR 18-SEP-1997; 97US-005263P.  
PR 18-SEP-1997; 97US-005266P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
PR 24-OCT-1997; 97US-0063121P.  
PR 28-OCT-1997; 97US-0063540P.  
PR 28-OCT-1997; 97US-0063541P.  
PR 28-OCT-1997; 97US-0063544P.  
PR 28-OCT-1997; 97US-0063564P.  
PR 29-OCT-1997; 97US-0063734P.  
PR 31-OCT-1997; 97US-0063870P.  
PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066772P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 18-DEC-1997; 97US-0068017P.  
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Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred No. 1,66-314; Indels 0; Gaps 0;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPYCTLTLYILMQLTGSAAAGPVKELVGSVGAATPEPLSKVQVDSIVTFTTTP 60  
1 MAGSPYCTLTLYILMQLTGSAAAGPVKELVGSVGAATPEPLSKVQVDSIVTFTTTP 60  
DB 61 VTIQPEGGTIIYQNNRERVDPPDGYSLKSLKKNDSGIYVGIYSSSLQDPSTOE 120  
61 VTIQPEGGTIIYQNNRERVDPPDGYSLKSLKKNDSGIYVGIYSSSLQDPSTOE 120  
QY 121 VLVHYEHLKPKYTMGLQSNKNGTCVTNLTCCMEHEGEDVIYTWKALGQANSHNGSIL 180  
121 VLVHYEHLKPKYTMGLQSNKNGTCVTNLTCCMEHEGEDVIYTWKALGQANSHNGSIL 180  
DB 121 VLVHYEHLKPKYTMGLQSNKNGTCVTNLTCCMEHEGEDVIYTWKALGQANSHNGSIL 180  
121 VLVHYEHLKPKYTMGLQSNKNGTCVTNLTCCMEHEGEDVIYTWKALGQANSHNGSIL 180  
QY 181 PISMRWGESDMFTICVARNPVSRNFSPIARLCEGAADDPSSMVLCLLVPLLSL 240  
181 PISMRWGESDMFTICVARNPVSRNFSPIARLCEGAADDPSSMVLCLLVPLLSL 240  
DB 181 PISMRWGESDMFTICVARNPVSRNFSPIARLCEGAADDPSSMVLCLLVPLLSL 240  
181 PISMRWGESDMFTICVARNPVSRNFSPIARLCEGAADDPSSMVLCLLVPLLSL 240  
QY 241 FVLGLPLWFLKREOREYIEEKKRVDCRETPICHSGENTYDITPHTRILKEDPA 300  
241 FVLGLPLWFLKREOREYIEEKKRVDCRETPICHSGENTYDITPHTRILKEDPA 300  
DB 241 FVLGLPLWFLKREOREYIEEKKRVDCRETPICHSGENTYDITPHTRILKEDPA 300  
241 FVLGLPLWFLKREOREYIEEKKRVDCRETPICHSGENTYDITPHTRILKEDPA 300  
QY 301 NTYSTVEIPIKKMNPNSLLTMDTPRLPAYENVI 335  
301 NTYSTVEIPIKKMNPNSLLTMDTPRLPAYENVI 335  
DB 301 NTYSTVEIPIKKMNPNSLLTMDTPRLPAYENVI 335  
301 NTYSTVEIPIKKMNPNSLLTMDTPRLPAYENVI 335

## RESULT 13

ABR65622  
ID ABR65622 standard; protein; 335 AA.

XX ABR65622;

DT 05-AUG-2003 (first entry)

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

XX Human; PRO; secreted protein; transmembrane protein;  
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
XX chondrocyte; proliferation; differentiation; cartilage disorder;  
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
XX liver; drug screening; transgenic animal; genetic analysis;  
XX antiarthritic; veterinary; gene therapy.

OS Homo sapiens.

PN US2003036159-A1.

XX 20-FEB-2003.

PD 02-JUL-2002; 2002US-00188773.

XX

PR 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
PR 24-OCT-1997; 97US-0063121P.  
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PR 18-SEP-1998; 98US-0101014P.  
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PR 23-SEP-1998; 98US-0101471P.  
PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101475P.  
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PR 25-SEP-1998; 98US-0101786P.  
PR 29-SEP-1998; 98US-0102207P.  
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PR 29-SEP-1998; 98US-0102330P.  
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PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.

Query Match 100.0%; Score 335; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1,6e-314;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VTIQPEGGTITIVQNNRRERVDPPDGYSIKLSKLNKNDGIIYVGIIYSSSLQGPSTQEX 120  
DB 61 VTIQPEGGTITIVQNNRRERVDPPDGYSIKLSKLNKNDGIIYVGIIYSSSLQGPSTQEX 120  
QY 121 VLAHVHLSKPKYTMGLQSNKNGTCVTNLTCCMEHEGEDIYTWKALGQANSHSGSL 180  
DB 121 VLAHVHLSKPKYTMGLQSNKNGTCVTNLTCCMEHEGEDIYTWKALGQANSHSGSL 180  
QY 181 PISMKGESDMTFCVARNPVSRNFSPIIARKLCEGAADDPSSMWLCLLVLPLLSL 240  
DB 181 PISMKGESDMTFCVARNPVSRNFSPIIARKLCEGAADDPSSMWLCLLVLPLLSL 240  
QY 241 FVLGLFLWFLKREOREEYIEKKRVDICRETPNICPHSGENTYDTPHTNRITLKEDPA 300  
DB 241 FVLGLFLWFLKREOREEYIEKKRVDICRETPNICPHSGENTYDTPHTNRITLKEDPA 300  
QY 301 NTYVSTVEIPKKMENPHSLTMDPTPLFAYENV 335  
DB 301 NTYVSTVEIPKKMENPHSLTMDPTPLFAYENV 335

RESULT 14

ID ABU9562 standard; protein; 335 AA.

XX ABU9562;

DT 09-AUG-2003 (first entry)

DE Human secreted/transmembrane protein (PRO) #96.

XX Human; secreted and transmembrane protein; PRO; TNF-alpha;

KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
cissue typing.

XX OS Homo sapiens.  
XX EN US2003040070-A1.  
XX  
XX 27-FEB-2003.  
XX  
PF 27-JUN-2002; 2002US-00184627.  
XX 18-SEP-1997; 97US-0059263P.  
XX 18-SEP-1997; 97US-0059266P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 21-OCT-1997; 97US-0063486P.  
XX 24-OCT-1997; 97US-0063120P.  
XX 24-OCT-1997; 97US-0063121P.  
XX 28-OCT-1997; 97US-0063540P.  
XX 28-OCT-1997; 97US-0063541P.  
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Job time : 58 secs



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: August 18, 2004, 16:06:16 ; Search time 19 Seconds

(Without alignments)  
910.247 Million cell updates/sec

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Minimum DB seq length: 0

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Post-processing: Listing first 700 summaries

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5	7	2.1	63	US-09-646-691B-10	Sequence 10, App1
6	7	2.1	67	US-09-543-681A-4733	Sequence 4733, Ap
7	7	2.1	97	US-09-886-319A-29	Sequence 29, App1
8	7	2.1	98	US-08-613-822-4	Sequence 4, App1
9	7	2.1	98	US-08-852-212-2	Sequence 2, App1
10	7	2.1	98	US-09-479-729B-4	Sequence 4, App1
11	7	2.1	98	US-09-261-201A-4	Sequence 4, App1
12	7	2.1	98	US-09-717-209-4	Sequence 2, App1
13	7	2.1	98	US-09-545-894-2	Sequence 2, App1
14	7	2.1	192	US-08-486-099-107	Sequence 107, App
15	7	2.1	192	US-08-360-107A-117	Sequence 117, App
16	7	2.1	192	US-08-484-223B-107	Sequence 107, App
17	7	2.1	192	US-08-919-597-107	Sequence 107, App
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21	7	2.1	192	US-08-485-264A-107	Sequence 107, App
22	7	2.1	192	US-08-474-349A-107	Sequence 107, App
23	7	2.1	192	US-08-470-896-107	Sequence 107, App
24	7	2.1	192	US-08-485-546A-107	Sequence 107, App
25	7	2.1	192	US-08-680-726A-72	Sequence 72, App1
26	7	2.1	208	US-09-092-409-72	Sequence 72, App1
27	7	2.1	229	US-09-078-691-4	Sequence 4, App1

28	7	2.1	244	US-09-328-352-4316	Sequence 4316, Ap
29	7	2.1	264	US-09-069-023-7	Sequence 7, App1
30	7	2.1	300	US-09-099-041A-4	Sequence 4, App1
31	7	2.1	300	US-09-245-281-4	Sequence 4, App1
32	7	2.1	300	US-09-207-359B-4	Sequence 4, App1
33	7	2.1	300	US-09-340-620A-4	Sequence 4, App1
34	7	2.1	300	US-09-865-364-4	Sequence 4, App1
35	7	2.1	303	US-09-632-947B-5	Sequence 5, App1
36	7	2.1	316	US-09-078-691-2	Sequence 2, App1
37	7	2.1	318	US-09-107-532A-6372	Sequence 6372, Ap
38	7	2.1	332	US-09-543-681A-6622	Sequence 6622, Ap
39	7	2.1	357	US-09-252-991A-32265	Sequence 32265, A
40	7	2.1	375	US-09-134-000C-4818	Sequence 4818, Ap
41	7	2.1	408	US-09-014-969-13	Sequence 13, App1
42	7	2.1	419	US-08-997-080-125	Sequence 125, App
43	7	2.1	419	US-08-997-362-125	Sequence 125, App
44	7	2.1	419	US-09-095-855-125	Sequence 125, App
45	7	2.1	419	US-09-324-542-125	Sequence 125, App
46	7	2.1	419	US-09-205-426-125	Sequence 125, App
47	7	2.1	427	US-09-134-000C-4837	Sequence 4837, Ap
48	7	2.1	439	US-09-282-305-6	Sequence 6, App1
49	7	2.1	439	US-09-883-720-6	Sequence 6, App1
50	7	2.1	467	US-09-489-039A-11144	Sequence 11144, A
51	7	2.1	472	US-09-107-532A-6117	Sequence 6117, Ap
52	7	2.1	478	US-09-069-023-4	Sequence 4, App1
53	7	2.1	530	US-09-069-023-3	Sequence 3, App1
54	7	2.1	531	US-09-069-023-1	Sequence 1, App1
55	7	2.1	539	US-09-800-170-16	Sequence 16, App1
56	7	2.1	540	US-09-019-942-1	Sequence 1, App1
57	7	2.1	540	US-09-099-041A-2	Sequence 2, App1
58	7	2.1	540	US-09-069-023-27	Sequence 27, App1
59	7	2.1	540	US-09-245-281-2	Sequence 2, App1
60	7	2.1	540	US-09-470-271-1	Sequence 1, App1
61	7	2.1	540	US-09-207-359B-2	Sequence 2, App1
62	7	2.1	540	US-09-340-620A-2	Sequence 2, App1
63	7	2.1	540	US-09-345-473E-28	Sequence 28, App1
64	7	2.1	540	US-09-865-364-2	Sequence 2, App1
65	7	2.1	540	US-09-748-537-1	Sequence 1, App1
66	7	2.1	666	US-09-252-991A-18949	Sequence 18949, A
67	7	2.1	650	US-09-310-463-2	Sequence 2, App1
68	7	2.1	650	US-08-842-248A-2	Sequence 2, App1
69	7	2.1	651	US-08-985-950-22	Sequence 22, App1
70	7	2.1	651	US-09-546-049-22	Sequence 22, App1
71	7	2.1	652	US-09-310-463-4	Sequence 4, App1
72	7	2.1	652	US-08-842-248A-4	Sequence 4, App1
73	7	2.1	670	US-08-997-080-178	Sequence 178, App
74	7	2.1	670	US-08-997-362-178	Sequence 178, App
75	7	2.1	670	US-09-095-855-178	Sequence 178, App
76	7	2.1	670	US-09-324-542-178	Sequence 178, App
77	7	2.1	670	US-09-205-426-178	Sequence 178, App
78	7	2.1	722	US-08-997-080-174	Sequence 174, App
79	7	2.1	722	US-08-997-362-174	Sequence 174, App
80	7	2.1	722	US-09-095-855-174	Sequence 174, App
81	7	2.1	722	US-09-324-542-174	Sequence 174, App
82	7	2.1	722	US-09-205-426-174	Sequence 174, App
83	7	2.1	963	US-08-637-002A-3	Sequence 3, App1
84	7	2.1	963	US-08-863-010-3	Sequence 3, App1
85	7	2.1	964	US-09-024-429-3	Sequence 3, App1
86	7	2.1	964	US-09-543-681A-5035	Sequence 5035, Ap
87	7	2.1	972	US-09-489-039A-11867	Sequence 11867, A
88	7	2.1	1019	US-08-271-364A-7	Sequence 7, App1
89	7	2.1	1019	US-08-222-715B-26	Sequence 26, App1
90	7	2.1	1085	US-08-431-080-28	Sequence 28, App1
91	7	2.1	1085	US-08-938-534-28	Sequence 28, App1
92	7	2.1	1085	US-09-345-294-28	Sequence 28, App1
93	7	2.1	1161	US-09-252-991A-28872	Sequence 28872, A
94	7	2.1	1290	US-09-150-460B-6	Sequence 6, App1
95	7	2.1	1291	US-09-150-460B-10	Sequence 10, App1
96	7	2.1	1291	US-09-220-641-5	Sequence 5, App1
97	7	2.1	1561	US-09-110-517-2	Sequence 2, App1
98	7	2.1	1561	US-09-248-588-66	Sequence 66, App1
99	6	1.8	12	US-08-836-075A-110	Sequence 130, App
100	6	1.8	18	US-09-470-830A-2	Sequence 2, App1

101	6	1.8	19	3	US-08-848-580-8	Sequence 8, Appl1	174	6	1.8	96	4	US-09-366-887A-9	Sequence 9, Appl1
102	6	1.8	19	4	US-08-488-123-8	Sequence 8, Appl1	175	6	1.8	97	2	US-08-467-822-40	Sequence 40, Appl1
103	6	1.8	19	4	US-09-470-830A-3	Sequence 3, Appl1	176	6	1.8	97	3	US-09-472-971-4	Sequence 4, Appl1
104	6	1.8	19	4	US-09-470-830A-4	Sequence 4, Appl1	177	6	1.8	97	3	US-08-432-697-40	Sequence 40, Appl1
105	6	1.8	19	5	PCT-US92-04537-4	Sequence 4, Appl1	177	6	1.8	97	3	US-08-466-248-40	Sequence 40, Appl1
106	6	1.8	20	4	US-09-470-830A-43	Sequence 43, Appl1	178	6	1.8	97	4	US-09-886-319A-11	Sequence 21, Appl1
107	6	1.8	21	3	US-08-488-580-9	Sequence 9, Appl1	180	6	1.8	97	4	US-09-545-894-13	Sequence 13, Appl1
108	6	1.8	21	3	US-08-488-123-9	Sequence 9, Appl1	181	6	1.8	97	4	US-09-545-894-16	Sequence 16, Appl1
109	6	1.8	21	5	PCT-US92-04537-5	Sequence 5, Appl1	182	6	1.8	98	3	US-08-776-971-11	Sequence 11, Appl1
110	6	1.8	23	3	US-07-927-391-7	Sequence 7, Appl1	183	6	1.8	98	3	US-08-776-971-44	Sequence 44, Appl1
111	6	1.8	25	4	US-09-690-454-200	Sequence 200, App	184	6	1.8	98	3	US-08-776-971-115	Sequence 115, App
112	6	1.8	28	4	US-08-848-580-10	Sequence 10, Appl	185	6	1.8	98	3	US-08-776-971-117	Sequence 117, App
113	6	1.8	28	4	US-09-149-476-322	Sequence 322, App	186	6	1.8	98	3	US-08-776-971-122	Sequence 122, App
114	6	1.8	28	4	US-09-149-476-509	Sequence 509, App	187	6	1.8	98	3	US-08-776-971-131	Sequence 131, App
115	6	1.8	28	4	US-08-488-123-10	Sequence 10, Appl	188	6	1.8	98	3	US-08-776-971-136	Sequence 136, App
116	6	1.8	28	5	PCT-US92-04537-6	Sequence 6, Appl1	189	6	1.8	99	1	US-08-127-499A-35	Sequence 35, Appl1
117	6	1.8	29	3	US-07-927-391-8	Sequence 8, Appl1	190	6	1.8	99	1	US-08-482-847-35	Sequence 35, Appl1
118	6	1.8	30	2	US-08-619-198-7	Sequence 8, Appl1	191	6	1.8	99	1	US-08-347-492B-8	Sequence 8, Appl1
119	6	1.8	33	3	US-07-927-391-9	Sequence 9, Appl1	192	6	1.8	99	1	US-08-480-449-18	Sequence 18, Appl1
120	6	1.8	33	3	US-08-789-333F-15	Sequence 15, Appl	193	6	1.8	99	1	US-08-480-449-19	Sequence 19, Appl1
121	6	1.8	33	3	US-09-169-015-25	Sequence 25, Appl	194	6	1.8	99	2	US-08-479-126B-5	Sequence 5, Appl1
122	6	1.8	33	3	US-09-133-944-15	Sequence 15, Appl	195	6	1.8	99	2	US-08-421-144A-5	Sequence 5, Appl1
123	6	1.8	33	4	US-09-208-827-16	Sequence 16, Appl	196	6	1.8	99	2	US-08-726-830A-5	Sequence 5, Appl1
124	6	1.8	33	4	US-08-787-738B-15	Sequence 15, Appl	197	6	1.8	99	2	US-08-660-542-18	Sequence 18, Appl1
125	6	1.8	33	4	US-09-157-748-18	Sequence 18, Appl	198	6	1.8	99	2	US-08-660-542-19	Sequence 19, Appl1
126	6	1.8	33	4	US-09-800-170-68	Sequence 68, Appl	199	6	1.8	99	2	US-08-798-143-8	Sequence 8, Appl1
127	6	1.8	33	4	US-09-626-581D-28	Sequence 28, Appl	200	6	1.8	99	3	US-07-927-391-24	Sequence 24, Appl1
128	6	1.8	33	4	US-09-415-765B-28	Sequence 28, Appl	201	6	1.8	99	3	US-08-995-156A-5	Sequence 5, Appl1
129	6	1.8	33	4	US-09-626-580C-28	Sequence 28, Appl	202	6	1.8	99	3	US-09-044-856A-5	Sequence 5, Appl1
130	6	1.8	33	4	US-09-749-959-24	Sequence 24, Appl	203	6	1.8	99	3	US-09-044-855A-5	Sequence 5, Appl1
131	6	1.8	40	3	US-10-043-074-16	Sequence 16, Appl	204	6	1.8	99	3	US-08-613-822-18	Sequence 18, Appl1
132	6	1.8	43	3	US-08-776-971-113	Sequence 113, App	205	6	1.8	99	3	US-08-928-383B-14	Sequence 14, Appl1
133	6	1.8	43	1	US-07-998-003A-57	Sequence 57, Appl	206	6	1.8	99	3	US-09-133-521-5	Sequence 5, Appl1
134	6	1.8	43	1	US-08-453-274B-57	Sequence 57, Appl	207	6	1.8	99	4	US-08-679-493A-152	Sequence 152, App
135	6	1.8	43	1	US-08-453-695A-57	Sequence 57, Appl	208	6	1.8	99	4	US-08-479-603-18	Sequence 18, Appl
136	6	1.8	43	1	US-08-268-161A-57	Sequence 57, Appl	209	6	1.8	99	4	US-08-479-603-19	Sequence 19, Appl1
137	6	1.8	43	2	US-08-453-702A-57	Sequence 57, Appl	210	6	1.8	99	4	US-09-419-281-5	Sequence 5, Appl1
138	6	1.8	43	3	US-09-099-639-57	Sequence 57, Appl	211	6	1.8	99	4	US-09-479-729B-18	Sequence 18, Appl1
139	6	1.8	43	5	PCT-US93-12588-57	Sequence 57, Appl	212	6	1.8	99	4	US-09-366-887A-10	Sequence 10, Appl1
140	6	1.8	43	5	PCT-US95-08071-57	Sequence 57, Appl	213	6	1.8	99	4	US-09-366-887A-17	Sequence 17, Appl
141	6	1.8	47	3	US-09-391-799-6	Sequence 6, Appl1	214	6	1.8	99	4	US-08-939-107-18	Sequence 18, Appl1
142	6	1.8	47	3	US-09-208-140-7	Sequence 6, Appl1	215	6	1.8	99	4	US-09-886-319A-22	Sequence 22, Appl1
143	6	1.8	49	3	US-09-208-140-19	Sequence 19, Appl	216	6	1.8	99	4	US-09-886-319A-30	Sequence 30, Appl1
144	6	1.8	49	3	US-09-208-140-31	Sequence 31, Appl	217	6	1.8	99	4	US-09-717-209-18	Sequence 18, Appl1
145	6	1.8	49	3	US-09-208-140-32	Sequence 32, Appl1	218	6	1.8	99	4	US-09-545-894-5	Sequence 5, Appl1
146	6	1.8	56	4	US-09-621-976-5480	Sequence 5480, App	219	6	1.8	99	4	US-09-545-894-7	Sequence 7, Appl1
147	6	1.8	56	4	US-09-621-976-6983	Sequence 6983, App	220	6	1.8	99	5	PCT-US96-10087-5	Sequence 5, Appl1
148	6	1.8	62	4	US-09-621-976-4988	Sequence 4988, App	221	6	1.8	99	6	5212073-2	Patent No. 5212073
149	6	1.8	65	4	US-09-543-681A-5670	Sequence 5670, App	222	6	1.8	103	3	US-08-894-173-77	Sequence 77, Appl1
150	6	1.8	67	4	US-09-621-976-6567	Sequence 6567, App	223	6	1.8	103	3	US-09-398-193-77	Sequence 77, Appl1
151	6	1.8	69	4	US-09-621-976-6740	Sequence 6740, App	224	6	1.8	103	4	US-09-084-303B-198	Sequence 198, App
152	6	1.8	73	4	US-09-543-681A-4655	Sequence 4655, App	225	6	1.8	104	3	US-08-744-419-2	Sequence 2, Appl1
153	6	1.8	74	3	US-08-905-223-294	Sequence 294, App	226	6	1.8	104	4	US-09-543-681A-8881	Sequence 4881, Appl
154	6	1.8	78	3	US-08-905-223-296	Sequence 296, App	227	6	1.8	104	4	US-09-545-894-4	Sequence 4, Appl1
155	6	1.8	79	4	US-09-621-976-5293	Sequence 5293, App	228	6	1.8	104	4	US-09-489-039A-13803	Sequence 13803, A
156	6	1.8	80	4	US-09-328-352-5464	Sequence 5464, App	229	6	1.8	107	4	US-09-489-039A-13627	Sequence 13627, A
157	6	1.8	82	4	US-09-540-236-3087	Sequence 3087, App	230	6	1.8	109	2	US-08-421-144A-7	Sequence 7, Appl1
158	6	1.8	82	4	US-09-489-039A-13580	Sequence 13580, A	231	6	1.8	109	2	US-07-927-391-16	Sequence 16, Appl1
159	6	1.8	83	3	US-08-776-971-45	Sequence 45, Appl1	232	6	1.8	109	3	US-08-679-493A-153	Sequence 153, App
160	6	1.8	83	3	US-08-776-971-124	Sequence 124, App	233	6	1.8	109	4	US-09-886-319A-71	Sequence 71, Appl1
161	6	1.8	83	3	US-08-776-971-137	Sequence 137, App	234	6	1.8	110	4	US-09-366-887A-13	Sequence 13, Appl1
162	6	1.8	85	4	US-09-328-352-6104	Sequence 6104, App	235	6	1.8	110	4	US-09-540-236-2945	Sequence 2945, App
163	6	1.8	87	4	US-09-288-143-96	Sequence 96, Appl1	236	6	1.8	112	4	US-09-489-039A-1254	Sequence 1254, A
164	6	1.8	89	4	US-09-543-681A-6121	Sequence 6121, App	237	6	1.8	114	3	US-08-894-173-97	Sequence 97, Appl1
165	6	1.8	92	4	US-09-366-887A-14	Sequence 14, Appl1	238	6	1.8	114	3	US-09-398-193-97	Sequence 97, Appl1
166	6	1.8	92	4	US-09-252-991A-28334	Sequence 28334, A	239	6	1.8	114	3	US-09-134-000C-3879	Sequence 3879, App
167	6	1.8	94	1	US-09-621-976-5285	Sequence 5285, App	240	6	1.8	116	3	US-09-188-930-121	Sequence 121, App
168	6	1.8	94	1	US-08-150-203A-5	Sequence 5, Appl1	241	6	1.8	116	3	US-09-312-283C-121	Sequence 121, App
169	6	1.8	94	1	US-08-454-730-5	Sequence 5, Appl1	242	6	1.8	117	3	US-09-489-039A-8566	Sequence 8566, App
170	6	1.8	94	4	US-08-949-788-5	Sequence 5, Appl1	243	6	1.8	118	3	US-09-098-789-1	Sequence 1, Appl1
171	6	1.8	94	4	US-09-621-976-6341	Sequence 6341, App	244	6	1.8	122	2	US-09-109-266-8	Sequence 8, Appl1
172	6	1.8	95	4	US-09-198-452A-1220	Sequence 1220, App	245	6	1.8	124	2	US-09-134-001C-2930	Sequence 2930, App
173	6	1.8	95	4	US-09-621-976-5712	Sequence 5712, App	246	6	1.8	125	1	US-08-473-981A-10	Sequence 10, Appl1

247	6	1.8	125	2	US-08-474-087-10	Sequence 10, Appl	320	6	1.8	217	4	US-09-252-991A-30641	Sequence 30641, A
248	6	1.8	125	4	US-09-543-681A-4730	Sequence 4730, Ap	321	6	1.8	218	1	US-08-463-115-92	Sequence 92, Appl
249	6	1.8	128	4	US-09-461-325-165	Sequence 165, App	322	6	1.8	218	1	US-08-465-388-92	Sequence 92, Appl
250	6	1.8	128	4	US-10-012-542-165	Sequence 165, App	323	6	1.8	222	4	US-09-589-733C-11	Sequence 11, Appl
251	6	1.8	133	4	US-09-252-991A-31726	Sequence 31726, A	324	6	1.8	222	2	US-08-594-189B-22	Sequence 22, Appl
252	6	1.8	134	4	US-09-252-991A-18396	Sequence 18396, A	325	6	1.8	223	4	US-09-465-901-12	Sequence 12, Appl
253	6	1.8	136	4	US-09-205-258-465	Sequence 465, App	326	6	1.8	227	4	US-09-593-887-16	Sequence 16, Appl
254	6	1.8	137	4	US-09-205-258-308	Sequence 308, App	327	6	1.8	230	4	US-09-187-789-7	Sequence 7, Appl
255	6	1.8	140	4	US-09-543-681A-6498	Sequence 6498, Ap	328	6	1.8	231	4	US-09-252-991A-25675	Sequence 25675, A
256	6	1.8	145	4	US-09-328-352-7720	Sequence 7720, Ap	329	6	1.8	232	1	US-08-425-763-2	Sequence 2, Appl
257	6	1.8	146	4	US-09-732-210-621	Sequence 621, App	330	6	1.8	232	2	US-07-934-373C-32	Sequence 32, Appl
258	6	1.8	147	4	US-09-355-160D-7	Sequence 7, Appl	331	6	1.8	232	3	US-08-437-642B-32	Sequence 32, Appl
259	6	1.8	149	3	US-08-836-075A-30	Sequence 30, Appl	332	6	1.8	232	3	US-08-811-757-2	Sequence 2, Appl
260	6	1.8	149	4	US-08-635-886C-283	Sequence 283, App	333	6	1.8	232	3	US-09-249-230-2	Sequence 2, Appl
261	6	1.8	149	4	US-08-974-690C-283	Sequence 283, App	334	6	1.8	232	5	PCT-US93-07883-32	Sequence 32, Appl
262	6	1.8	151	4	US-09-564-329A-15	Sequence 15, Appl	335	6	1.8	237	4	US-09-107-532A-6553	Sequence 6553, Ap
263	6	1.8	155	4	US-09-107-532A-6942	Sequence 6942, Ap	336	6	1.8	238	2	US-08-768-964-7	Sequence 7, Appl
264	6	1.8	156	4	US-09-646-028-4	Sequence 4, Appl	337	6	1.8	238	3	US-09-005-299-7	Sequence 7, Appl
265	6	1.8	156	4	US-09-148-545-136	Sequence 136, App	338	6	1.8	238	3	US-09-515-431-7	Sequence 7, Appl
266	6	1.8	157	3	US-08-872-855-6	Sequence 6, Appl	339	6	1.8	238	4	US-09-149-476-485	Sequence 485, App
267	6	1.8	157	3	US-08-981-392-68	Sequence 68, Appl	340	6	1.8	241	4	US-09-187-789-5	Sequence 7889, Ap
268	6	1.8	157	4	US-09-252-991A-22516	Sequence 22516, A	341	6	1.8	242	4	US-09-187-789-5	Sequence 5, Appl
269	6	1.8	158	4	US-09-252-991A-26205	Sequence 26205, A	342	6	1.8	242	4	US-09-252-991A-24652	Sequence 24652, A
270	6	1.8	159	4	US-09-489-039A-12575	Sequence 12575, A	343	6	1.8	244	4	US-09-724-623-82	Sequence 82, Appl
271	6	1.8	166	3	US-08-916-576B-6	Sequence 6, Appl	344	6	1.8	245	3	US-09-413-814-6	Sequence 6, Appl
272	6	1.8	166	4	US-09-213-293D-18	Sequence 18, Appl	345	6	1.8	245	4	US-08-426-630-20	Sequence 20, Appl
273	6	1.8	168	1	US-08-193-577-9	Sequence 9, Appl	346	6	1.8	246	4	US-09-198-452A-22	Sequence 22, Appl
274	6	1.8	170	4	US-09-205-258-1011	Sequence 1011, Ap	347	6	1.8	248	4	US-09-482-273-126	Sequence 126, App
275	6	1.8	171	4	US-09-646-028-9	Sequence 9, Appl	348	6	1.8	252	4	US-09-252-991A-11553	Sequence 17553, A
276	6	1.8	172	4	US-09-252-991A-23876	Sequence 23876, A	349	6	1.8	254	3	US-09-310-463-36	Sequence 36, Appl
277	6	1.8	172	4	US-09-198-452A-1195	Sequence 1195, Ap	350	6	1.8	254	3	US-09-240-915-7	Sequence 7, Appl
278	6	1.8	174	2	US-08-768-964-13	Sequence 13, Appl	351	6	1.8	254	3	US-09-591-435-7	Sequence 7, Appl
279	6	1.8	174	3	US-09-005-299-13	Sequence 13, Appl	352	6	1.8	256	4	US-09-543-681A-4282	Sequence 4282, Ap
280	6	1.8	174	3	US-09-515-431-13	Sequence 13, Appl	353	6	1.8	257	1	US-07-781-355-2	Sequence 2, Appl
281	6	1.8	176	3	US-09-309-317-2	Sequence 2, Appl	354	6	1.8	257	1	US-08-287-959-4	Sequence 4, Appl
282	6	1.8	177	4	US-09-252-991A-20614	Sequence 20614, A	355	6	1.8	258	4	US-09-252-991A-25067	Sequence 25067, A
283	6	1.8	182	4	US-09-107-532A-5701	Sequence 5701, A	356	6	1.8	258	4	US-09-252-991A-29435	Sequence 29435, A
284	6	1.8	183	4	US-08-858-207A-401	Sequence 401, App	357	6	1.8	260	4	US-09-252-991A-22320	Sequence 22320, A
285	6	1.8	181	4	US-08-671-548C-30	Sequence 30, Appl	358	6	1.8	263	2	US-08-768-964-2	Sequence 2, Appl
286	6	1.8	183	4	US-08-671-548C-20	Sequence 20, Appl	359	6	1.8	263	3	US-09-005-299-2	Sequence 2, Appl
287	6	1.8	183	4	US-08-671-548C-36	Sequence 36, Appl	360	6	1.8	263	3	US-09-515-431-2	Sequence 2, Appl
288	6	1.8	184	4	US-08-671-548C-26	Sequence 26, Appl	361	6	1.8	263	3	US-09-198-452A-1063	Sequence 1063, Ap
289	6	1.8	186	3	US-08-981-392-35	Sequence 35, Appl	362	6	1.8	265	4	US-09-310-463-34	Sequence 34, Appl
290	6	1.8	186	4	US-09-328-352-5098	Sequence 5098, Ap	363	6	1.8	266	2	US-07-857-2248-40	Sequence 40, Appl
291	6	1.8	189	2	US-08-768-964-12	Sequence 12, Appl	364	6	1.8	266	3	US-09-147-550-11	Sequence 11, Appl
292	6	1.8	189	3	US-09-005-299-12	Sequence 12, Appl	365	6	1.8	266	3	US-09-557-917-11	Sequence 11, Appl
293	6	1.8	189	3	US-09-515-431-12	Sequence 12, Appl	366	6	1.8	266	4	US-09-543-681A-5904	Sequence 5904, Ap
294	6	1.8	199	4	US-09-252-991A-30003	Sequence 30003, A	367	6	1.8	267	4	US-09-134-000C-5723	Sequence 5723, Ap
295	6	1.8	204	1	US-08-185-432-8	Sequence 8, Appl	368	6	1.8	272	3	US-08-690-095-1	Sequence 1, Appl
296	6	1.8	205	4	US-09-134-000C-3913	Sequence 3913, Ap	369	6	1.8	272	3	US-09-113-789-1	Sequence 1, Appl
297	6	1.8	206	4	US-09-362-737-51	Sequence 51, Appl	370	6	1.8	274	4	US-09-570-367C-19	Sequence 19, Appl
298	6	1.8	206	4	US-09-562-737-55	Sequence 55, Appl	371	6	1.8	274	4	US-09-252-991A-27466	Sequence 27466, A
299	6	1.8	206	4	US-09-562-737-56	Sequence 56, Appl	372	6	1.8	274	4	US-09-515-524-19	Sequence 19, Appl
300	6	1.8	206	4	US-09-562-737-57	Sequence 57, Appl	373	6	1.8	274	4	US-09-515-524-19	Sequence 19, Appl
301	6	1.8	206	4	US-09-562-737-58	Sequence 58, Appl	374	6	1.8	274	4	US-09-515-524-19	Sequence 19, Appl
302	6	1.8	207	4	US-09-489-847-285	Sequence 285, App	375	6	1.8	274	4	US-09-570-367C-2	Sequence 2, Appl
303	6	1.8	209	3	US-08-235-836C-32	Sequence 32, Appl	376	6	1.8	278	4	US-09-570-367C-21	Sequence 21, Appl
304	6	1.8	210	4	US-09-697-367-10	Sequence 10, Appl	377	6	1.8	278	4	US-09-915-524-2	Sequence 2, Appl
305	6	1.8	210	4	US-09-134-001C-4790	Sequence 4790, Ap	378	6	1.8	278	4	US-09-915-524-21	Sequence 21, Appl
306	6	1.8	211	4	US-09-252-991A-25965	Sequence 25965, A	379	6	1.8	282	4	US-09-247-890-16	Sequence 16, Appl
307	6	1.8	212	4	US-08-158-353-4	Sequence 4, Appl	380	6	1.8	282	4	US-09-724-969-16	Sequence 16, Appl
308	6	1.8	212	2	US-08-753-121-1	Sequence 1, Appl	381	6	1.8	282	4	US-09-724-969-16	Sequence 16, Appl
309	6	1.8	212	2	US-08-878-957-34	Sequence 34, Appl	382	6	1.8	282	4	US-09-134-000C-4468	Sequence 4468, Ap
310	6	1.8	212	3	US-09-196-293-11	Sequence 11, Appl	383	6	1.8	283	4	US-09-504-615-106	Sequence 106, App
311	6	1.8	212	3	US-08-209-603B-11	Sequence 11, Appl	384	6	1.8	287	4	US-09-310-463-32	Sequence 32, Appl
312	6	1.8	212	3	US-08-235-836C-34	Sequence 34, Appl	385	6	1.8	287	4	US-09-252-991A-30447	Sequence 30447, A
313	6	1.8	212	4	US-09-216-066-1	Sequence 1, Appl	386	6	1.8	287	4	US-09-489-039A-14187	Sequence 14187, A
314	6	1.8	212	4	US-09-711-546-11	Sequence 11, Appl	387	6	1.8	288	4	US-09-489-039A-12218	Sequence 12218, A
315	6	1.8	213	2	US-08-763-121-3	Sequence 3, Appl	388	6	1.8	288	4	US-09-252-991A-26267	Sequence 26267, A
316	6	1.8	213	4	US-09-216-066-3	Sequence 3, Appl	389	6	1.8	297	4	US-09-632-947B-4	Sequence 4, Appl
317	6	1.8	214	4	US-09-187-789-9	Sequence 9, Appl	390	6	1.8	298	4	US-09-232-160-17	Sequence 17, Appl
318	6	1.8	216	4	US-09-489-039A-7265	Sequence 7265, Ap	391	6	1.8	298	4	US-09-252-991A-23700	Sequence 23700, A
319	6	1.8	217	4	US-09-690-454-196	Sequence 196, App	392	6	1.8	298	4	US-09-800-729-87	Sequence 87, Appl

393	6	1.8	298	4	US-09-800-729-121	Sequence 121, App	466	6	1.8	352	2	US-08-933-750C-46	Sequence 46, App1
394	6	1.8	298	4	US-09-582-934-2	Sequence 2, App1	467	6	1.8	352	3	US-09-234-613-46	Sequence 46, App1
395	6	1.8	299	4	US-09-310-463-30	Sequence 30, App1	468	6	1.8	352	4	US-09-252-991A-25209	Sequence 25209, A
396	6	1.8	300	4	US-09-543-681A-6670	Sequence 6670, Ap	469	6	1.8	353	4	US-09-543-681A-7190	Sequence 7190, Ap
397	6	1.8	301	4	US-09-107-532A-4953	Sequence 4953, Ap	470	6	1.8	353	2	US-08-394-189B-20	Sequence 20, App1
398	6	1.8	301	4	US-09-582-934-1	Sequence 1, App1	471	6	1.8	356	4	US-09-198-452A-526	Sequence 526, App
399	6	1.8	302	4	US-09-874-923-122	Sequence 122, App	472	6	1.8	358	4	US-09-934-901-8	Sequence 8, App1
400	6	1.8	303	4	US-08-185-432-5	Sequence 5, App1	473	6	1.8	361	4	US-09-668-097A-16	Sequence 36, App1
401	6	1.8	304	4	US-09-632-947B-7	Sequence 7, App1	474	6	1.8	362	4	US-09-134-001C-5403	Sequence 5403, Ap
402	6	1.8	304	4	US-09-489-039A-11906	Sequence 11906, A	475	6	1.8	363	4	US-09-252-991A-18016	Sequence 18016, A
403	6	1.8	305	4	US-09-540-236-3603	Sequence 3603, Ap	476	6	1.8	363	4	US-09-252-991A-25052	Sequence 25052, A
404	6	1.8	308	4	US-09-252-991A-20337	Sequence 20337, A	477	6	1.8	364	4	US-09-205-258-1008	Sequence 1008, Ap
405	6	1.8	309	1	US-08-729-202-1	Sequence 1, App1	478	6	1.8	364	4	US-09-417-485D-49	Sequence 49, App
406	6	1.8	309	3	US-08-896-371-1	Sequence 2, App1	479	6	1.8	370	4	US-08-724-224-2	Sequence 2, App1
407	6	1.8	309	3	US-08-996-338-22	Sequence 22, App1	480	6	1.8	371	1	US-08-225-477B-8	Sequence 8, App1
408	6	1.8	309	4	US-09-556-972-22	Sequence 22, App1	481	6	1.8	371	5	US-09-148-545-259	Sequence 259, App
409	6	1.8	310	4	US-09-252-991A-16914	Sequence 16914, A	482	6	1.8	371	5	PCT-US95-04353-8	Sequence 8, App1
410	6	1.8	311	4	US-09-222-939-8	Sequence 8, App1	483	6	1.8	372	4	US-09-071-035-102	Sequence 102, App
411	6	1.8	311	4	US-09-252-991A-28068	Sequence 28068, A	484	6	1.8	372	4	US-09-252-991A-28586	Sequence 28586, A
412	6	1.8	311	4	US-09-543-681A-4963	Sequence 4963, Ap	485	6	1.8	372	4	US-09-252-991A-30132	Sequence 30132, A
413	6	1.8	312	2	US-10-023-528-8	Sequence 8, App1	486	6	1.8	377	3	US-08-888-077A-27	Sequence 27, App1
414	6	1.8	312	2	US-08-808-931-22	Sequence 22, App1	487	6	1.8	377	4	US-09-665-479A-16	Sequence 16, App1
415	6	1.8	312	3	US-08-808-323-22	Sequence 22, App1	488	6	1.8	378	1	US-08-225-477B-9	Sequence 9, App1
416	6	1.8	312	3	US-09-050-603A-22	Sequence 22, App1	489	6	1.8	378	5	PCT-US95-04353-9	Sequence 9, App1
417	6	1.8	312	3	US-09-102-420B-22	Sequence 22, App1	490	6	1.8	379	4	US-09-489-039A-11991	Sequence 11991, A
418	6	1.8	312	4	US-09-497-698-22	Sequence 22, App1	491	6	1.8	382	4	US-09-029-333-2	Sequence 2, App1
419	6	1.8	312	4	US-09-107-532A-6219	Sequence 6219, Ap	492	6	1.8	384	3	US-08-946-026-27	Sequence 27, App1
420	6	1.8	313	3	US-09-347-803-25	Sequence 25, App1	493	6	1.8	386	4	US-09-724-623-70	Sequence 70, App1
421	6	1.8	313	4	US-09-252-991A-22411	Sequence 22411, A	494	6	1.8	387	1	US-08-123-161A-10	Sequence 10, App1
422	6	1.8	313	4	US-09-252-991A-24305	Sequence 24305, A	495	6	1.8	387	1	US-08-123-161A-12	Sequence 12, App1
423	6	1.8	314	4	US-09-107-532A-4919	Sequence 4919, Ap	496	6	1.8	387	1	US-08-483-278-10	Sequence 10, App1
424	6	1.8	315	4	US-07-757-390-8	Sequence 8, App1	497	6	1.8	387	1	US-08-483-278-12	Sequence 12, App1
425	6	1.8	315	1	US-08-442-282-8	Sequence 8, App1	498	6	1.8	387	4	US-09-134-001C-3625	Sequence 3625, Ap
426	6	1.8	315	2	US-08-442-281-8	Sequence 8, App1	499	6	1.8	390	1	US-07-817-920-6	Sequence 6, App1
427	6	1.8	315	2	US-08-939-727-8	Sequence 8, App1	500	6	1.8	390	1	US-08-117-006-6	Sequence 6, App1
428	6	1.8	315	4	US-09-252-991A-25763	Sequence 25763, A	501	6	1.8	390	1	US-08-216-594-6	Sequence 6, App1
429	6	1.8	316	4	US-09-252-991A-18829	Sequence 18829, A	502	6	1.8	390	2	US-08-461-812-4	Sequence 4, App1
430	6	1.8	317	4	US-09-252-991A-22489	Sequence 22489, A	503	6	1.8	390	2	US-08-157-185-15	Sequence 15, App1
431	6	1.8	318	4	US-09-134-001C-3852	Sequence 3852, Ap	504	6	1.8	390	3	US-08-281-526B-15	Sequence 15, App1
432	6	1.8	319	4	US-09-134-000C-5242	Sequence 5242, Ap	505	6	1.8	390	4	US-09-450-790A-15	Sequence 15, App1
433	6	1.8	324	4	US-09-252-991A-24664	Sequence 24664, A	506	6	1.8	390	4	US-09-332-837-15	Sequence 15, App1
434	6	1.8	329	1	US-08-225-477B-3	Sequence 3, App1	507	6	1.8	390	4	US-09-371-705-4	Sequence 4, App1
435	6	1.8	329	2	US-08-562-535C-4	Sequence 4, App1	508	6	1.8	390	5	PCT-US93-00149-6	Sequence 6, App1
436	6	1.8	329	2	US-08-742-605D-4	Sequence 4, App1	509	6	1.8	395	4	US-09-328-352-6660	Sequence 6660, Ap
437	6	1.8	329	3	US-09-259-294-4	Sequence 4, App1	510	6	1.8	395	4	US-09-543-681A-6203	Sequence 6203, Ap
438	6	1.8	329	5	US-09-489-039A-10276	Sequence 10276, A	511	6	1.8	398	1	US-07-757-390-6	Sequence 6, App1
439	6	1.8	329	5	PCT-US95-04353-3	Sequence 3, App1	512	6	1.8	398	1	US-08-370-542-6	Sequence 6, App1
440	6	1.8	331	1	US-08-356-180-3	Sequence 3, App1	513	6	1.8	398	1	US-08-442-282-6	Sequence 6, App1
441	6	1.8	331	1	US-07-757-390-7	Sequence 7, App1	514	6	1.8	398	1	US-08-542-358-6	Sequence 6, App1
442	6	1.8	332	1	US-08-442-282-7	Sequence 7, App1	515	6	1.8	398	1	US-08-442-281-6	Sequence 6, App1
443	6	1.8	332	1	US-08-442-281-7	Sequence 7, App1	516	6	1.8	398	2	US-08-939-727-6	Sequence 6, App1
444	6	1.8	332	2	US-08-039-727-7	Sequence 7, App1	517	6	1.8	398	3	US-09-018-351-6	Sequence 6, App1
445	6	1.8	333	4	US-09-198-452A-652	Sequence 652, App	518	6	1.8	398	4	US-09-328-352-6411	Sequence 4411, Ap
446	6	1.8	334	4	US-09-252-991A-18120	Sequence 18120, A	519	6	1.8	399	4	US-09-134-000C-4500	Sequence 4500, Ap
447	6	1.8	334	4	US-09-252-991A-22395	Sequence 22395, A	520	6	1.8	406	4	US-09-252-991A-31178	Sequence 31178, A
448	6	1.8	335	1	US-07-947-130-3	Sequence 3, App1	521	6	1.8	402	4	US-09-134-001C-3544	Sequence 3544, Ap
449	6	1.8	335	1	US-08-421-822-3	Sequence 3, App1	522	6	1.8	409	3	US-09-258-754-449	Sequence 4449, App
450	6	1.8	335	1	US-08-421-823-3	Sequence 3, App1	523	6	1.8	410	4	US-09-252-991A-22340	Sequence 22340, A
451	6	1.8	335	4	US-09-543-681A-7733	Sequence 7733, Ap	524	6	1.8	411	4	US-09-543-681A-7404	Sequence 7404, Ap
452	6	1.8	337	2	US-09-013-634-2	Sequence 2, App1	525	6	1.8	412	1	US-08-349-696-21	Sequence 21, App1
453	6	1.8	340	4	US-09-543-681A-5967	Sequence 5967, Ap	526	6	1.8	412	1	US-08-233-009-21	Sequence 21, App1
454	6	1.8	342	4	US-09-071-035-104	Sequence 104, App	527	6	1.8	412	2	US-08-560-231-21	Sequence 21, App1
455	6	1.8	344	3	US-09-110-116-4	Sequence 4, App1	528	6	1.8	412	3	US-09-080-704A-21	Sequence 21, App1
456	6	1.8	345	4	US-09-252-991A-16669	Sequence 16669, A	529	6	1.8	412	4	US-09-800-274-5	Sequence 5, App1
457	6	1.8	346	4	US-09-724-224-6	Sequence 6, App1	530	6	1.8	413	4	US-09-252-991A-20866	Sequence 20866, A
458	6	1.8	346	5	PCT-US96-10602-2	Sequence 2, App1	531	6	1.8	414	4	US-09-543-681A-4330	Sequence 4330, Ap
459	6	1.8	347	1	US-08-857-076-100	Sequence 100, App	532	6	1.8	414	4	US-09-489-039A-10428	Sequence 10428, A
460	6	1.8	349	1	US-08-118-270-7	Sequence 7, App1	533	6	1.8	415	1	US-07-757-390-5	Sequence 5, App1
461	6	1.8	349	5	PCT-US93-08528-7	Sequence 7, App1	534	6	1.8	415	1	US-08-442-282-5	Sequence 5, App1
462	6	1.8	350	4	US-09-161-241-9	Sequence 9, App1	535	6	1.8	415	1	US-08-442-281-5	Sequence 5, App1
463	6	1.8	350	4	US-09-907-794A-236	Sequence 236, App	536	6	1.8	415	2	US-08-939-727-5	Sequence 5, App1
464	6	1.8	350	4	US-09-905-125A-236	Sequence 236, App	537	6	1.8	415	4	US-09-886-039A-23	Sequence 23, App1
465	6	1.8	350	4	US-09-902-775A-236	Sequence 236, App	538	6	1.8	417	4	US-09-489-039A-12272	Sequence 12272, A

539	6	1.8	419	3	US-08-974-691-3	Sequence 3, Appl1	612	6	1.8	487	4	US-09-489-039A-12980	Sequence 12980, A
540	6	1.8	419	4	US-09-705-448-10	Sequence 10, Appl	613	6	1.8	489	4	US-08-983-502-9	Sequence 9, Appl1
541	6	1.8	421	4	US-09-543-681A-7791	Sequence 791, Ap	614	6	1.8	489	4	US-09-516-747-9	Sequence 9, Appl1
542	6	1.8	423	2	US-08-290-731C-10	Sequence 10, Appl	615	6	1.8	489	5	PCT-US96-10521-9	Sequence 9, Appl1
543	6	1.8	423	2	US-08-290-731C-11	Sequence 11, Appl	616	6	1.8	495	4	US-09-328-352-4637	Sequence 4637, Ap
544	6	1.8	423	3	US-08-855-910-13	Sequence 13, Appl	617	6	1.8	500	4	US-09-107-532A-4085	Sequence 4085, Ap
545	6	1.8	424	4	US-09-328-352-4199	Sequence 4199, Ap	618	6	1.8	503	2	US-08-394-1898-2	Sequence 2, Appl1
546	6	1.8	426	4	US-09-352-991A-20025	Sequence 20025, A	619	6	1.8	503	3	US-08-258-2878-35	Sequence 35, Appl
547	6	1.8	427	4	US-09-134-000C-5142	Sequence 5142, Ap	620	6	1.8	503	3	US-08-258-2878-36	Sequence 36, Appl
548	6	1.8	430	4	US-08-956-171E-5244	Sequence 5244, Ap	621	6	1.8	503	3	US-08-368-704C-2	Sequence 2, Appl1
549	6	1.8	433	4	US-09-252-991A-20728	Sequence 20728, A	622	6	1.8	503	3	US-08-368-704C-35	Sequence 35, Appl
550	6	1.8	436	4	US-09-252-991A-22081	Sequence 22081, A	623	6	1.8	503	3	US-08-368-704C-36	Sequence 36, Appl
551	6	1.8	437	4	US-09-252-991A-32048	Sequence 32048, A	624	6	1.8	503	3	US-08-368-704C-35	Sequence 35, Appl
552	6	1.8	440	2	US-08-808-931-24	Sequence 24, Appl	625	6	1.8	503	3	US-08-740-223A-11	Sequence 11, Appl
553	6	1.8	440	3	US-08-808-931-24	Sequence 24, Appl	626	6	1.8	503	4	US-09-709-188-11	Sequence 11, Appl
554	6	1.8	440	3	US-09-050-603A-24	Sequence 24, Appl	627	6	1.8	503	4	US-08-724-3780-10	Sequence 10, Appl
555	6	1.8	440	3	US-09-102-4208-24	Sequence 24, Appl	628	6	1.8	503	4	US-08-999-689A-6	Sequence 6, Appl1
556	6	1.8	440	3	US-09-497-698-24	Sequence 24, Appl	629	6	1.8	503	4	US-09-291-289-12	Sequence 12, Appl
557	6	1.8	442	4	US-09-252-991A-30607	Sequence 30607, A	630	6	1.8	503	5	PCT-US93-05701-19	Sequence 19, Appl
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559	6	1.8	450	4	US-09-489-039A-9246	Sequence 9246, Ap	632	6	1.8	505	2	US-08-394-1898-5	Sequence 5, Appl1
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561	6	1.8	454	2	US-07-934-373C-22	Sequence 22, Appl	634	6	1.8	505	5	PCT-US93-05705-5	Sequence 5, Appl1
562	6	1.8	454	3	US-08-437-642B-22	Sequence 22, Appl	635	6	1.8	507	4	US-09-252-991A-22432	Sequence 23432, A
563	6	1.8	454	3	US-08-929-329-8	Sequence 8, Appl1	636	6	1.8	509	2	US-08-665-926-8	Sequence 8, Appl1
564	6	1.8	454	4	US-08-146-206C-22	Sequence 22, Appl	637	6	1.8	509	3	US-08-740-223A-10	Sequence 10, Appl
565	6	1.8	454	4	US-09-705-686-22	Sequence 22, Appl	638	6	1.8	509	4	US-09-202-491-2	Sequence 2, Appl1
566	6	1.8	454	5	PCT-US93-07832-22	Sequence 22, Appl	639	6	1.8	509	4	US-09-202-491-3	Sequence 3, Appl1
567	6	1.8	455	4	US-09-540-236-2325	Sequence 2325, Ap	640	6	1.8	509	4	US-09-709-188-10	Sequence 10, Appl
568	6	1.8	456	4	US-09-328-352-6174	Sequence 6174, Ap	641	6	1.8	509	4	US-09-328-352-6488	Sequence 6488, Ap
569	6	1.8	459	2	US-08-870-518-4	Sequence 4, Appl1	642	6	1.8	510	1	US-08-278-635B-4	Sequence 4, Appl1
570	6	1.8	459	3	US-08-836-567-4	Sequence 4, Appl1	643	6	1.8	510	1	US-08-471-961-4	Sequence 4, Appl1
571	6	1.8	459	4	US-09-606-304-4	Sequence 4, Appl1	644	6	1.8	510	4	US-09-345-109C-4	Sequence 4, Appl1
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590	6	1.8	468	4	US-09-134-001C-3999	Sequence 3999, Ap	663	6	1.8	522	4	US-09-198-452A-480	Sequence 480, Ap
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593	6	1.8	468	4	US-10-039-785-1	Sequence 1, Appl1	666	6	1.8	528	3	US-08-808-323-10	Sequence 10, Appl
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595	6	1.8	474	4	US-09-340-236-3598	Sequence 3598, Ap	668	6	1.8	528	3	US-09-102-420B-10	Sequence 10, Appl
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597	6	1.8	479	4	US-09-540-236-2292	Sequence 2292, Ap	670	6	1.8	528	4	US-09-010-147B-20	Sequence 20, Appl
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605	6	1.8	483	3	US-09-071-296-6	Sequence 6, Appl1	678	6	1.8	536	4	US-09-328-352-4594	Sequence 4594, Ap
606	6	1.8	483	3	US-09-196-268-6	Sequence 6, Appl1	679	6	1.8	537	1	US-08-472-028A-2	Sequence 2, Appl1
607	6	1.8	483	4	US-09-191-598-6	Sequence 6, Appl1	680	6	1.8	537	2	US-08-808-931-2	Sequence 2, Appl1
608	6	1.8	484	4	US-09-328-352-4849	Sequence 4849, Ap	681	6	1.8	537	3	US-08-808-323-2	Sequence 2, Appl1
609	6	1.8	487	4	US-09-724-224-8	Sequence 8, Appl1	682	6	1.8	537	3	US-09-050-603A-2	Sequence 2, Appl1
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697 6 1.8 541 4 US-09-578-178-2 Sequence 2, Appl1
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## ALIGNMENTS

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RESULT 1
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; Sequence 213, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
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; ORGANISM: Homo sapiens
US-09-907-794A-213
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Best Local Similarity 100.0%; Pred. No. 16;
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; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR FILING DATE: 1999-09-08  
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PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
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NUMBER OF SEQ ID NOS: 423  
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Patent No. 6686451  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvarole, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,775A  
CURRENT FILING DATE: 2001-07-10  
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PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
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PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 213  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-902-775A-213

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Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
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Sequence 31174, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142

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; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31174

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DB 312 LVGSVGA 319

RESULT 5  
US-09-646-691B-10  
; Sequence 10, Application US/09646691B

; Patent No. 6642353  
; GENERAL INFORMATION:  
; APPLICANT: McCONNELL, Stephen, J. and SPINELLA, Dominic, G.  
; TITLE OF INVENTION: PEPTIDE LIGANDS FOR THE ERYTHROPOIETIN  
; RECEPTOR

; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Gen-Probe Incorporated  
; STREET: 10210 Genetic Center Drive  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92121

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/646,691B  
; FILING DATE: 20-SEP-2000  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Giltzmaecher, Christine A  
; REGISTRATION NUMBER: 40,627  
; REFERENCE/DOCKET NUMBER: CB9701-A01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-410-8926  
; TELEFAX: 619-410-8928  
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6642353e  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-646-691B-10

Query Match 2.1%; Score 7; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TGSASG 24  
| | | | |  
DB 37 TGSASG 43

RESULT 6  
US-09-543-681A-4733  
; Sequence 4733, Application US/09543681A

; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709,1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 4733  
; LENGTH: 67  
; TYPE: PR  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-4733

Query Match 2.1%; Score 7; DB 4; Length 67;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 LLSLFL 243  
| | | | |  
DB 60 LLSLFL 66

RESULT 7  
US-09-886-319A-29  
; Sequence 29, Application US/09886319A

; Patent No. 6586185  
; GENERAL INFORMATION:  
; APPLICANT: Wolf, Eckard  
; APPLICANT: Werner, Sabine  
; APPLICANT: Halle, Jörn-Peter  
; APPLICANT: Regenhagen, Johannes  
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for  
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound  
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically  
; TITLE OF INVENTION: Active Substances  
; FILE REFERENCE: 50125/014002  
; CURRENT APPLICATION NUMBER: US/09/886,319A  
; CURRENT FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: US 60/222,081  
; PRIOR FILING DATE: 2000-08-01  
; PRIOR APPLICATION NUMBER: DE 10030149.5  
; PRIOR FILING DATE: 2000-06-20

; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 97  
; TYPE: PR  
; ORGANISM: Mus musculus  
US-09-886-319A-29

Query Match 2.1%; Score 7; DB 4; Length 97;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLICLL 233  
| | | | |  
DB 6 VLICLL 12

RESULT 8  
US-08-613-922-4  
; Sequence 4, Application US/08613822  
; Patent No. 6174995  
; GENERAL INFORMATION:  
; APPLICANT: Li, Haodong  
; TITLE OF INVENTION: Human Chemokine Polypeptides  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESSES:



ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/613,822  
FILING DATE: 23-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Milistein, Larry S  
REGISTRATION NUMBER: 34,679  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-613-822-4

Query Match 2.1%; Score 7; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLICLL 233  
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DB 6 VLICLL 12

RESULT 9  
US-08-852-212-2  
Sequence 2, Application US/08852212  
Patent No. 6290948  
GENERAL INFORMATION:  
APPLICANT: White et al.  
FILE REFERENCE: P501  
CURRENT APPLICATION NUMBER: US/08/852,212  
CURRENT FILING DATE: 1997-05-06  
EARLIER APPLICATION NUMBER: 60/017,871  
EARLIER FILING DATE: 1996-05-14  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-852-212-2

Query Match 2.1%; Score 7; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLICLL 233  
|||||  
DB 6 VLICLL 12

RESULT 10  
US-09-479-7298-4  
Sequence 4, Application US/094797298  
Patent No. 6391589  
GENERAL INFORMATION:  
APPLICANT: Olsen, et al

TITLE OF INVENTION: Human Chemokine Beta-10 Mutant Polypeptides  
FILE REFERENCE: P504  
CURRENT APPLICATION NUMBER: US/09/479,7298  
CURRENT FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: PCT/US94/09484  
PRIOR FILING DATE: 1994-08-23  
PRIOR APPLICATION NUMBER: 08/458,355  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: 08/462,967  
PRIOR FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: 60/115,439  
PRIOR FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 4  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-479-7298-4

Query Match 2.1%; Score 7; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLICLL 233  
|||||  
DB 6 VLICLL 12

RESULT 11  
US-09-261-201A-4  
Sequence 4, Application US/09261201A  
Patent No. 6458349  
GENERAL INFORMATION:  
APPLICANT: Li et al.  
TITLE OF INVENTION: Polynucleotides Encoding Chemokine B-4  
FILE REFERENCE: P132P1D1  
CURRENT APPLICATION NUMBER: US/09/261,201A  
CURRENT FILING DATE: 1999-03-03  
PRIOR APPLICATION NUMBER: 08/458,355  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: PCT/US94/09484  
PRIOR FILING DATE: 1994-08-23  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 4  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-261-201A-4

Query Match 2.1%; Score 7; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLICLL 233  
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DB 6 VLICLL 12

RESULT 12  
US-09-717-209-4  
Sequence 4, Application US/09717209  
Patent No. 6673344  
GENERAL INFORMATION:  
APPLICANT: Li, Haodong  
TITLE OF INVENTION: Human Chemokine Polypeptides  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD

COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/717,209  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/613,822  
FILING DATE: 23-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Millesfeld, Larry S  
REGISTRATION NUMBER: 34,679  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-717-209-4

Query Match 2.1%; Score 7; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VLICLL 233  
Db 6 VLICLL 12

RESULT 13  
US-09-545-894-2  
Sequence 2, Application US/09545894  
Patent No. 6673915  
GENERAL INFORMATION:  
APPLICANT: Luster, Andrew D.  
Garcia-Zepeda, Eduardo A.  
Sarafl, Mindy N.  
TITLE OF INVENTION: MCP-4 AND MCP-5: NOVEL CHEMOKINES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/545,894  
FILING DATE: 07-APR-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/940,687  
FILING DATE: 30-SEP-1997  
APPLICATION NUMBER: 60/027,128  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bleker-Brady, Kristina  
REGISTRATION NUMBER: 39,109  
REFERENCE/DOCKET NUMBER: 00786/293002  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-545-894-2

Query Match 2.1%; Score 7; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VLICLL 233  
Db 6 VLICLL 12

RESULT 14  
US-08-486-099-107  
Sequence 107, Application US/08486099  
Patent No. 6013263  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
TITLE OF INVENTION: B VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 209  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,099  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-486-099-107

Query Match 2.1%; Score 7; DB 3; Length 192;  
Best Local Similarity 100.0%; Pred. No. 83;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 LTCLLV 234  
| | | | |

Db 139 LTCLLV 145

## RESULT 15

US-08-360-107A-117

/ Sequence 117, Application US/08360107A  
/ Patent No. 6017536

/ GENERAL INFORMATION:

/ APPLICANT: Bolognesi, Dani P.

/ APPLICANT: Matthews, Thomas J.

/ APPLICANT: Wild, Carl T.

/ APPLICANT: Barney, Shawn O.

/ APPLICANT: Lambert, Dennis M.

/ APPLICANT: Petteaway, Stephen R.

/ APPLICANT: Langlois, Alphonse J.

/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

/ TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

/ NUMBER OF SEQUENCES: 149

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Pennie & Edmonds

/ STREET: 1155 Avenue of the Americas

/ CITY: New York

/ STATE: New York

/ COUNTRY: USA

/ ZIP: 10036-2711

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/360,107A

/ FILING DATE: 20-DEC-1994

/ CLASSIFICATION: 435

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Coruzzi, Laura A.

/ REGISTRATION NUMBER: 30,742

/ REFERENCE/DOCKET NUMBER: 7872-013

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (212) 790-9090

/ TELEFAX: (212) 869-9741/8864

/ TELEX: 66141 PENNIE

/ INFORMATION FOR SEQ ID NO: 117:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 192 amino acids

/ TYPE: amino acid

/ STRANDEDNESS:

/ TOPOLOGY: unknown

/ MOLECULE TYPE: protein

/ US-08-360-107A-117

Query Match 2.1%; Score 7; DB 3; Length 192;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 LTCLLV 234  
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Db 139 LTCLLV 145

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: August 18, 2004, 16:08:36 ; Search time 47 Seconds  
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2237.566 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 335  
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Scoring table:

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Searched: 1292805 seqs, 313927144 residues

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Minimum DB seq length: 0  
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Published Applications AA:\*

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- 10: /cgn2\_6/prodata/2/pubppaa/US09C\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/2/pubppaa/US09C\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/prodata/2/pubppaa/US09C\_PUBCOMB.pep.\*
- 13: /cgn2\_6/prodata/2/pubppaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/2/pubppaa/US10C\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/2/pubppaa/US10C\_NEW\_PUB.pep.\*
- 16: /cgn2\_6/prodata/2/pubppaa/US60\_NEW\_PUB.pep.\*
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- 18: /cgn2\_6/prodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	335	100.0	335	9	US-09-989-722-253
3	335	100.0	335	9	US-09-989-723-253
4	335	100.0	335	9	US-09-989-729-253
5	335	100.0	335	9	US-09-989-727-253
6	335	100.0	335	9	US-09-989-731-253
7	335	100.0	335	9	US-09-989-732-253
8	335	100.0	335	9	US-09-989-732-253
9	335	100.0	335	9	US-09-991-073-253
10	335	100.0	335	9	US-09-980-442-253
11	335	100.0	335	9	US-09-991-163-253
12	335	100.0	335	9	US-09-993-604-253
13	335	100.0	335	9	US-09-990-456-253
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16	335	100.0	335	9	US-09-989-293A-253	Sequence 253, App
17	335	100.0	335	9	US-09-989-735-253	Sequence 253, App
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;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1,3e-305;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 3

US-09-989-723-253  
Sequence 253, Application US/09989723  
Patent No. US20020072092A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
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;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
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;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerltisen, Mary E.  
;; APPLICANT: Goddard, Audrey  
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;; APPLICANT: Kijavini, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel

;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC62  
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PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred.No. 1.3e-305; Indels 0; Gaps 0;

Matches 335; Conservative 0; Mismatches 0;

QY 1 MAGSPCTCLTLYILMOLTSAGPVEKLVGSVGAATVPLKSKVQVDSIVTFTNTPL 60  
DB 1 MASSPTCLTLYILMOLTSAGPVEKLVGSVGAATVPLKSKVQVDSIVTFTNTPL 60  
QY 61 VTIQPEGGTLIVTQNNRERVDPEPDGYSIKLSKLNKNSGIYVGIYSSLSQPSIOEX 120  
DB 61 VTIQPEGGTLIVTQNNRERVDPEPDGYSIKLSKLNKNSGIYVGIYSSLSQPSIOEX 120  
QY 121 VLVHYEHLKPKXTMGLQSNKGTCTVNTLTCCHEHEBEDVITYWKALQGANESHGSL 180  
DB 121 VLVHYEHLKPKXTMGLQSNKGTCTVNTLTCCHEHEBEDVITYWKALQGANESHGSL 180  
QY 181 PISMRGSDMTFCIARNDVSRNFSSTILARKLCEGAADDPSSNVLLCLLVLPLLSL 240  
DB 181 PISMRGSDMTFCIARNDVSRNFSSTILARKLCEGAADDPSSNVLLCLLVLPLLSL 240  
QY 241 FVLGLFLMPLKREOREYIEKKRVDICRETPNICPHSGENTERYDITPHNRTILKEDPA 300  
DB 241 FVLGLFLMPLKREOREYIEKKRVDICRETPNICPHSGENTERYDITPHNRTILKEDPA 300  
QY 301 NTYVSTVEIPKKNENPHSLTTPDTPRLAYENVI 335  
DB 301 NTYVSTVEIPKKNENPHSLTTPDTPRLAYENVI 335

#### RESULT 4

US-09-989-279-253  
Sequence 253, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C56  
CURRENT APPLICATION NUMBER: US/09/989,279  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
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PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.3e-305;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSPTCLTILYIMOLTGSAAGPVKELVGSVGAVTFPLKSKVKQVDSIWTFTTTL 60  
DB 1 MASSPTCLTILYIMOLTGSAAGPVKELVGSVGAVTFPLKSKVKQVDSIWTFTTTL 60  
QY VTIOPEGGTLIVONRREKREVDPPDGGYSLKSLKKNDSGIYVVGYSLSLOOPISTQY 120  
DB 61 VTIOPEGGTLIVONRREKREVDPPDGGYSLKSLKKNDSGIYVVGYSLSLOOPISTQY 120  
QY VLVHYEHLSPKVTYMGQSNKNGTCVTNLTCMEHGEDEVITYWKALGOANSHNGSIL 180  
DB 121 VLVHYEHLSPKVTYMGQSNKNGTCVTNLTCMEHGEDEVITYWKALGOANSHNGSIL 180  
QY PISMRGESDMTFCVARNVSRNFSPIIARKLCCEAADDPPSSMWLCLLLVPLLSL 240  
DB 181 PISMRGESDMTFCVARNVSRNFSPIIARKLCCEAADDPPSSMWLCLLLVPLLSL 240  
QY FVYGLFMPFKRERQEBYIEKKRVDICRETPNICPSGENTEXTDTPHTNRITLIKEDPA 300  
DB 241 FVYGLFMPFKRERQEBYIEKKRVDICRETPNICPSGENTEXTDTPHTNRITLIKEDPA 300  
QY NTVYSTVEIKPKMENPHSLLTMPDTPPLFAVENYI 335  
DB 301 NTVYSTVEIKPKMENPHSLLTMPDTPPLFAVENYI 335

RESULT 5  
US-09-989-727-253  
Sequence 253, Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deonoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Gerlitsen, Mary E.  
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APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C65  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/065311  
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.3e-305; Indels 0; Gaps 0;  
Matches 335; Conservative 0; Mismatches 0;

Qy 1 MAGSPTCLTLYIYIMQLGSAAGVKEIVSGAVTFFPKSKYKQVDSITWTFNTPL 60  
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Qy VTIOPEGTTIIVTONRNERVDPPDGGYSLKLSKLKNDSGIYVGVISSSIQPSTOEY 120  
Db VTIOPEGTTIIVTONRNERVDPPDGGYSLKLSKLKNDSGIYVGVISSSIQPSTOEY 120  
Qy VLAHYEHLISKRVMTGLQSNKNGCTVNTLTCMEHGEEDVIYTWKALQOANESHNGSIL 180  
Db VLAHYEHLISKRVMTGLQSNKNGCTVNTLTCMEHGEEDVIYTWKALQOANESHNGSIL 180



QY 181 PISRMGESDWTFCVARNPVSRNPFSSPILARKICEGAADPDSSMWLLCILLVPLILSL 240  
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QY 301 NTYVSTVEIPKPMENPHSLTMTPTPLPAYENVI 335  
DB 301 NTYVSTVEIPKPMENPHSLTMTPTPLPAYENVI 335  
RESULT 6  
US-09-989-731-253  
Sequence 253, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Napier, Mary A.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989, 731  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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;; PRIOR APPLICATION NUMBER: 60/089947  
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;; PRIOR APPLICATION NUMBER: 60/090863  
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;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1.3e-305;

Matches: 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAGSPFCLTLIYIIMOLTSAAAGPVKEIVGSGAVTFPLSKSKYKOYDSIWTENTPPL 60  
Db 1 MAGSPFCLTLIYIIMOLTSAAAGPVKEIVGSGAVTFPLSKSKYKOYDSIWTENTPPL 60  
Qy 61 VTIOPEGGTIIYTONRRNRVDPDGGYSLKLSKLUKNDSCGIYVGIYSSSIQOPSTOEY 120  
Db 61 VTIOPEGGTIIYTONRRNRVDPDGGYSLKLSKLUKNDSCGIYVGIYSSSIQOPSTOEY 120  
Qy 121 VHAHYEHLSPKVTYMGLOSNKNGTCVTNLTCMEHGEEDVIYTWKALQQAANESHNGSL 180  
Db 121 VHAHYEHLSPKVTYMGLOSNKNGTCVTNLTCMEHGEEDVIYTWKALQQAANESHNGSL 180  
Qy 181 PLSMRWGESDMTFICVARNPVSRNPSPIARKLCEGAADDPDSMWLLCLLVLPLLSL 240  
Db 181 PLSMRWGESDMTFICVARNPVSRNPSPIARKLCEGAADDPDSMWLLCLLVLPLLSL 240  
Qy 241 FVLGLFLWFLKRRGEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTIILKEDPA 300  
Db 241 FVLGLFLWFLKRRGEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTIILKEDPA 300  
Qy 301 NTVYSTVEIPKXENPHSLTTPDTPRLPAYENVI 335  
Db 301 NTVYSTVEIPKXENPHSLTTPDTPRLPAYENVI 335

RESULT 7  
US-09-989-732-253  
; Sequence 253, Application US/09989732  
; Patent No. US20020123463A1  
; GENERAL INFORMATION:  
; APPLICANT: Aehkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Goddard, Audrey E.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PLC57  
; CURRENT APPLICATION NUMBER: US/09/989,732  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25



;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1,3e-305;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTLLIYILMQLTSSAAGPYKELVGSVGAATPEPLSKVKQVDSIWTFTTTL 60  
DB 1 MAGSPCTLLIYILMQLTSSAAGPYKELVGSVGAATPEPLSKVKQVDSIWTFTTTL 60  
QY 61 VTIOPEGTTIYVQNNRRERVDPPDGYSIKLSKLNKNDSGIYVGIYSSSLQGPSTQRY 120  
DB 61 VTIOPEGTTIYVQNNRRERVDPPDGYSIKLSKLNKNDSGIYVGIYSSSLQGPSTQRY 120  
QY 121 VLAHYEHLSPKVTWGLQSNKNGCTVTNLTCCMEHGEEDVIYTWKALQQAANESHNGSIL 180  
DB 121 VLAHYEHLSPKVTWGLQSNKNGCTVTNLTCCMEHGEEDVIYTWKALQQAANESHNGSIL 180  
QY 181 PISMRWGSDDMTFICVARNPVSRNFPSSPILARKLCEGAADDPSSMVLCLLIVPLLISL 240  
DB 181 PISMRWGSDDMTFICVARNPVSRNFPSSPILARKLCEGAADDPSSMVLCLLIVPLLISL 240  
QY 241 FVLGLFLWFLKREOREEYIEKKRVDICRETPNICPHSGENTYDITPHNTRTILKEDPA 300  
DB 241 FVLGLFLWFLKREOREEYIEKKRVDICRETPNICPHSGENTYDITPHNTRTILKEDPA 300  
QY 301 NTYVSTVEIPKKMENPHSLTMPDTPRLPAYENVI 335  
DB 301 NTYVSTVEIPKKMENPHSLTMPDTPRLPAYENVI 335

## RESULT 8

US-09-745-605-4  
; Sequence 4, Application US/09745605  
; Patent No. US20020123617A1  
; GENERAL INFORMATION:  
; APPLICANT: Stirling, Gary C.  
; APPLICANT: Stirling, Joshua N.  
; TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2,  
; FILE REFERENCE: DB13NP  
; CURRENT APPLICATION NUMBER: US/09/745,605  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/172,025  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-745-605-4

Query Match 100.0%; Score 335; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred. No. 1,3e-305;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VTIOPEGTTIYVQNNRRERVDPPDGYSIKLSKLNKNDSGIYVGIYSSSLQGPSTQRY 120  
DB 61 VTIOPEGTTIYVQNNRRERVDPPDGYSIKLSKLNKNDSGIYVGIYSSSLQGPSTQRY 120

QY 121 VLAHYEHLSPKVTWGLQSNKNGCTVTNLTCCMEHGEEDVIYTWKALQQAANESHNGSIL 180  
DB 121 VLAHYEHLSPKVTWGLQSNKNGCTVTNLTCCMEHGEEDVIYTWKALQQAANESHNGSIL 180  
QY 181 PISMRWGSDDMTFICVARNPVSRNFPSSPILARKLCEGAADDPSSMVLCLLIVPLLISL 240  
DB 181 PISMRWGSDDMTFICVARNPVSRNFPSSPILARKLCEGAADDPSSMVLCLLIVPLLISL 240  
QY 241 FVLGLFLWFLKREOREEYIEKKRVDICRETPNICPHSGENTYDITPHNTRTILKEDPA 300  
DB 241 FVLGLFLWFLKREOREEYIEKKRVDICRETPNICPHSGENTYDITPHNTRTILKEDPA 300  
QY 301 NTYVSTVEIPKKMENPHSLTMPDTPRLPAYENVI 335  
DB 301 NTYVSTVEIPKKMENPHSLTMPDTPRLPAYENVI 335

## RESULT 9

US-09-991-073-253  
; Sequence 253, Application US/0991073  
; Patent No. US20020127576A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertschen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Auecin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC15  
; CURRENT APPLICATION NUMBER: US/09/991,073  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607



; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;  
Best Local Similarity 100.0%; Pred No. 1.3e-305;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTLLIYLWQLTGSAASGPVKELVGSGAVTPEPLKSKVQVDSIWTFTTPL 60  
1 MAGSPCTCLTLLIYLWQLTGSAASGPVKELVGSGAVTPEPLKSKVQVDSIWTFTTPL 60

QY 61 VTIQPEGGTITIVQNNRRVRPDDGYSLSKLSKLNKNSGIVYVGIYSSLOQPESTQY 120  
61 VTIQPEGGTITIVQNNRRVRPDDGYSLSKLSKLNKNSGIVYVGIYSSLOQPESTQY 120

QY 121 VLVHYHLSKPKYTMGLQSNKNGTCVTNLTCCEHGEEDVITYWKALGQANESHNGSTL 180  
121 VLVHYHLSKPKYTMGLQSNKNGTCVTNLTCCEHGEEDVITYWKALGQANESHNGSTL 180

QY 181 PISMRWGESDMTFCVARNPVSRNFSPPILARKLCEGAADDPDSSWVLLCLLVPLLLSL 240  
181 PISMRWGESDMTFCVARNPVSRNFSPPILARKLCEGAADDPDSSWVLLCLLVPLLLSL 240

QY 241 FVLGLFLWFLKREKREYIEKKRVDICRETPNICHSGBNTBYDTIPIHTNRTILKEDPA 300  
241 FVLGLFLWFLKREKREYIEKKRVDICRETPNICHSGBNTBYDTIPIHTNRTILKEDPA 300

QY 301 NTYVSTVEIPIKKMENPHSLLTMPDTPRLFAVENVI 335  
301 NTYVSTVEIPIKKMENPHSLLTMPDTPRLFAVENVI 335

Db 301 NTYVSTVEIPIKKMENPHSLLTMPDTPRLFAVENVI 335

RESULT 10  
US-09-990-442-253  
; Sequence 253, Application US/09990442  
; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertlisen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C8  
; CURRENT APPLICATION NUMBER: US/09/990,442  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
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; PRIOR FILING DATE: 1998-06-02  
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; PRIOR APPLICATION NUMBER: 60/087759  
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; PRIOR FILING DATE: 1998-06-16  
; PRIOR APPLICATION NUMBER: 60/089532

;; PRIOR FILING DATE: 1998-06-17  
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;; PRIOR APPLICATION NUMBER: 60/089948  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089952  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090246  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;  
Best local Similarity 100.0%; Pred. No. 1,3e-305; Indels 0; Gaps 0;  
Matches 335; Conservative 0; Mismatches 0;

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Db 61 VTIQPEGGTIIYTONRNRERVPDPDGYSLKSLKKNDSGIYVYGIYSSSLQOPSTOEX 120  
Qy 121 VHHVYEHLSKPYXTMGLQSNKNGTCVTNLTCMEHGEEDVYITWKALGQANSHNGSIL 180  
Db 121 VHHVYEHLSKPYXTMGLQSNKNGTCVTNLTCMEHGEEDVYITWKALGQANSHNGSIL 180  
Qy 181 PLSMRGSDMTFICARNPVSRNPSPIIARLTCGADDDPSSWVLLCLLVPLLLSL 240  
Db 181 PLSMRGSDMTFICARNPVSRNPSPIIARLTCGADDDPSSWVLLCLLVPLLLSL 240  
Qy 241 FVLGLFLWFLKREROEYIEKKRVYDICKETPNICPHSGENTETDITPHTNRILKEDPA 300  
Db 241 FVLGLFLWFLKREROEYIEKKRVYDICKETPNICPHSGENTETDITPHTNRILKEDPA 300  
Qy 301 NTYVSTVEIIPKQENPHSLITMPDTPRLPAYENVI 335  
Db 301 NTYVSTVEIIPKQENPHSLITMPDTPRLPAYENVI 335

RESULT 11  
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Sequence 253, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Gerlitsen, Mary E.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

1 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
2 FILE REFERENCE: P2730P1C17  
3 CURRENT APPLICATION NUMBER: US/09/991,163  
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38	PRIOR FILING DATE: 1998-07-07
39	PRIOR APPLICATION NUMBER: 60/092162
40	PRIOR FILING DATE: 1998-07-09

Query Match	100.0%;	Score 335;	DB 9;	Length 335;
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Db	61	VTIQPEGGTIIYTONRNRERVDVFPDGGYSLKLSKLSKKNDSGIYVVGYSSSLQDPSTQEY	120
Qy	121	VLAHYEHLKPKYTMGLQSNKNGTCVTNI,TCOMEHGEEDVIYWKALGOANESHNGSIL	180
Db	121	VLAHYEHLKPKYTMGLQSNKNGTCVTNLTCOMEHGEEDVIYWKALGOANESHNGSIL	180
Qy	181	PISMRGESSDMTFICVARNPVSRNFSPLIARKLCEGAADPDSSMYLLCLLYPLILSL	240
Db	181	PISMRGESSDMTFICVARNPVSRNFSPLIARKLCEGAADPDSSMYLLCLLYPLILSL	240
Qy	241	FVLGLFLMFLKKEBQBEYIEKKRVDICRETPNICPHSGENTERTDITPHNRTILAKEDPA	300
Db	241	FVLGLFLMFLKKEBQBEYIEKKRVDICRETPNICPHSGENTERTDITPHNRTILAKEDPA	300
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Db	301	NTLYSTVELPKQKQENHSLITMPDPRIFAENYI	335

RESULT 13  
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; Sequence 253, Application US/09990456

Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumaas, Daniel  
APPLICANT: Tumaas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC22  
CURRENT APPLICATION NUMBER: US/09/990,456  
CURRENT FILING DATE: 2001-11-14  
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/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09
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Qy 121 VLAHYEHLSPKRYTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWALGOANESHNGSL 180
Db 121 VLAHYEHLSPKRYTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWALGOANESHNGSL 180
Qy 181 PLSMWGBSDMTFICVARNPVSRNFSPIIARKLCEGADDDSSMVLICLLVPLILSL 240
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/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Geider, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
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/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tanas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C55
/ CURRENT FILING DATE: 2001-11-19
/ PRIOR APPLICATION NUMBER: US/09/989,721
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## RESULT 15

US-09-992-598-253

Sequence 253, Application US/09992598

Patent No. US20020160384A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Baton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerltzen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

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APPLICANT: Stewart, Timothy A.

APPLICANT: Tunas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PLC20

CURRENT APPLICATION NUMBER: US/09/992,598

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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;  
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Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 NTYVSTVEIPKKNENPHSLTMPDTPRLFAVENVI 335  
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Search completed: August 18, 2004, 16:14:16  
Job time : 49 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2004, 16:13:22 ; Search time 17 seconds  
(without alignments)  
1895.339 Million cell updates/sec

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Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 700 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2.7	9	156	2 H72621	hypothetical prote
2	2.7	9	2464	1 QRMSP1	microtubule-associ
3	2.4	8	173	2 S76681	hypothetical prote
4	2.4	8	286	2 A82159	hypothetical prote
5	2.4	8	705	2 S18733	glutinin high mole
6	2.4	8	1117	2 S38673	desmoglein 2 - hum
7	2.1	7	105	2 T29918	hypothetical prote
8	2.1	7	161	2 E71866	hypothetical prote
9	2.1	7	170	2 AE1817	hypothetical prote
10	2.1	7	179	2 F97283	ribosomal protein
11	2.1	7	179	2 F83305	hypothetical prote
12	2.1	7	182	2 F97499	hypothetical prote
13	2.1	7	184	2 I40220	hypothetical prote
14	2.1	7	189	2 H70416	hypothetical prote
15	2.1	7	199	2 T45543	hypothetical prote
16	2.1	7	220	2 E75285	hypothetical prote
17	2.1	7	228	2 T47847	hypothetical prote
18	2.1	7	238	2 G69820	hypothetical prote
19	2.1	7	238	2 C82864	conserved hypochet
20	2.1	7	239	2 F69996	amino acid ABC tra
21	2.1	7	239	2 T51270	hypothetical prote
22	2.1	7	266	2 C87367	flagellar biosynth
23	2.1	7	274	2 G84218	cysteine synthase
24	2.1	7	290	2 A88616	protein T25C8.3 [i
25	2.1	7	301	2 T52549	probable thiosulfa
26	2.1	7	301	2 D83970	UDP-N-acetylglucos
27	2.1	7	302	2 E75414	PectN-related prote
28	2.1	7	303	2 A43727	UDP-N-acetylglucos
29	2.1	7	305	2 G96962	UDP-N-acetylglucos

30	2.1	312	1	LPRT	apolipoprotein E p
31	2.1	316	2	G95161	UDP-N-acetylglucos
32	2.1	316	2	P98027	UDP-N-acetylglucos
33	2.1	331	2	C89469	protein F07G6.1 [i
34	2.1	331	2	E84299	hypothetical prote
35	2.1	351	2	C82755	conserved hypochet
36	2.1	356	2	S14396	cytochrome-c oxida
37	2.1	362	2	S68471	asparaginase [EC 3
38	2.1	367	2	S41024	hypothetical prote
39	2.1	369	2	T21392	hypothetical prote
40	2.1	377	2	H89717	protein C18B12.2 [i
41	2.1	379	2	S49614	cycH protein - Rhi
42	2.1	381	2	T11776	ubiquinol-cytochro
43	2.1	381	2	T11312	ubiquinol-cytochro
44	2.1	410	2	B81744	poly(A) polymerase
45	2.1	413	2	T48089	hypothetical prote
46	2.1	418	2	F64059	tryptophan transpo
47	2.1	428	2	AD0675	membrane transport
48	2.1	433	2	S45856	probable membrane
49	2.1	443	2	AB2719	conserved hypochet
50	2.1	448	2	UC2305	glucuronate permease
51	2.1	454	2	T19380	hypothetical prote
52	2.1	458	2	F69123	efflux pump antibi
53	2.1	463	2	A69905	conserved hypochet
54	2.1	464	2	AG1146	beta-glucosidase h
55	2.1	464	2	AG1505	beta-glucosidase h
56	2.1	467	2	A99498	hypothetical prote
57	2.1	475	2	T47480	hypothetical prote
58	2.1	480	2	F97500	tolerance to colic
59	2.1	492	2	D87606	sensor histidine k
60	2.1	501	2	H95859	probable ABC trans
61	2.1	508	2	E96804	probable thioredox
62	2.1	513	2	B84391	DNA damage--inducib
63	2.1	512	2	AB2671	cytochrome-c oxida
64	2.1	586	1	VCLJMP	env polyprotein -
65	2.1	587	1	B54354	calnexin precursor
66	2.1	591	2	B54354	calnexin precursor
67	2.1	591	2	C54354	copper resistance
68	2.1	605	2	S52253	hypothetical prote
69	2.1	643	2	B72602	conserved hypochet
70	2.1	646	2	D82493	hypothetical prote
71	2.1	675	2	T22323	NADH2 dehydrogenas
72	2.1	730	2	T13792	acylaminoacyl-pept
73	2.1	732	1	JC4655	hypothetical prote
74	2.1	797	2	T50072	probable cell divi
75	2.1	799	2	H71255	probable helicase
76	2.1	829	2	T40239	penicillin-binding
77	2.1	914	2	I40529	exonuclease ABC, c
78	2.1	943	2	F95021	glycine cleavage s
79	2.1	943	2	C97893	glycine cleavage s
80	2.1	954	2	AF2756	glycine decarboxyl
81	2.1	954	2	E97537	hypothetical prote
82	2.1	957	2	F91100	glycine dehydrogen
83	2.1	957	2	B85946	glycine dehydrogen
84	2.1	957	2	S36834	iso-leucine--cRNA 11
85	2.1	957	2	S36834	glycine dehydrogen
86	2.1	958	2	AC0873	hypothetical prote
87	2.1	958	2	E82994	kinasin homolog f2
88	2.1	959	2	AB0111	IFN1 protein - yea
89	2.1	997	2	T32814	hypothetical prote
90	2.1	1002	2	S62035	fligiticlin--I homol
91	2.1	1002	2	JN0124	hypothetical prote
92	2.1	1032	2	S53571	period protein hom
93	2.1	1070	2	T06733	period protein hom
94	2.1	1085	2	S55352	DNA-directed DNA p
95	2.1	1166	2	T15628	surface layer-asso
96	2.1	1268	2	A49674	hypothetical prote
97	2.1	1277	2	T15109	hypothetical prote
98	2.1	1290	2	T00018	period protein hom
99	2.1	1291	2	T00019	period protein hom
100	2.1	1312	2	S68593	DNA-directed DNA p
101	2.1	1345	2	T29090	surface layer-asso
102	2.1	1355	2	T22552	hypothetical prote
103	2.1	1487	2	S15904	alpha-1 protease

103	7	2.1	1552	2	T05408	hypothetical prote
104	7	2.1	1560	2	T02885	peroxisome prolif
105	7	2.1	1585	2	AE2916	NAD-glucamate dehy
106	7	2.1	1585	2	H97690	NAD-glucamate dehy
107	7	2.1	1630	2	S61535	nucleotide-binding
108	7	2.1	2787	2	S45416	TBL1 protein - yea
109	7	2.1	3973	2	S71612	hypothetical prote
110	7	2.1	4545	1	S25111	alpha-2-macroglobu
111	6	1.8	30	2	S157689	ubiquitin1-cytochro
112	6	1.8	32	2	S21547	T-cell receptor al
113	6	1.8	36	2	H64507	hypothetical prote
114	6	1.8	39	2	C90523	hypothetical prote
115	6	1.8	52	2	C60232	T-cell surface gly
116	6	1.8	56	2	C69044	hypothetical prote
117	6	1.8	57	2	D95852	hypothetical prote
118	6	1.8	60	2	B28918	hypothetical prote
119	6	1.8	61	2	T01086	nodulin-14 precurs
120	6	1.8	66	2	C89925	hypothetical prote
121	6	1.8	70	2	A42155	hypothetical prote
122	6	1.8	72	2	C83219	hypothetical prote
123	6	1.8	73	2	T26110	hypothetical prote
124	6	1.8	74	2	T13199	hypothetical prote
125	6	1.8	75	2	C95204	hypothetical prote
126	6	1.8	77	2	AG2343	hypothetical prote
127	6	1.8	82	2	C81350	hypothetical prote
128	6	1.8	83	2	JC7607	prolactin-releasin
129	6	1.8	86	2	AC2117	hypothetical prote
130	6	1.8	92	2	T64109	mercury reductase
131	6	1.8	93	2	T45245	hypothetical prote
132	6	1.8	95	2	S68231	FHG22 protein prec
133	6	1.8	95	2	T49793	hypothetical prote
134	6	1.8	96	1	A42281	symblonin syms - p
135	6	1.8	96	1	ZEBRG4	gene B protein - p
136	6	1.8	96	2	JC4518	heat-shock protein
137	6	1.8	96	2	B64076	chaperonin groBS -
138	6	1.8	96	2	C82048	chaperonin, 10 Kd
139	6	1.8	96	2	AB4932	chaperonin groES -
140	6	1.8	97	1	BVRCGS	10 Kd chaperonin
141	6	1.8	97	2	A48093	monocytic cytochrome
142	6	1.8	97	2	JC5770	chaperonin groBS-1
143	6	1.8	97	2	AB6110	chaperonin mopB [6
144	6	1.8	97	2	C91269	chaperonin GroES (
145	6	1.8	97	2	AD1045	GroES protein [imp
146	6	1.8	97	2	E97266	glu-tRNA amidotran
147	6	1.8	98	2	S41828	NADH2 dehydrogenas
148	6	1.8	98	2	S24920	NADH2 dehydrogenas
149	6	1.8	98	2	T11488	NADH2 dehydrogenas
150	6	1.8	98	2	A39296	monocyte chemotatr
151	6	1.8	99	1	JC5295	monocyte chemotatr
152	6	1.8	99	2	JC2336	monocyte chemotatr
153	6	1.8	99	2	JC2136	monocyte chemotatr
154	6	1.8	99	2	A60299	monocyte chemotatr
155	6	1.8	99	2	JC2417	monocyte chemotatr
156	6	1.8	100	2	E64929	NADH2 dehydrogenase
157	6	1.8	100	2	C91024	NADH dehydrogenase
158	6	1.8	100	2	D85868	NADH dehydrogenase
159	6	1.8	100	2	AD0310	NADH2 dehydrogenas
160	6	1.8	100	2	AE0796	NADH2 dehydrogenas
161	6	1.8	100	2	B69846	hypothetical prote
162	6	1.8	101	2	S37068	NADH2 dehydrogenas
163	6	1.8	101	2	S64222	probable membrane
164	6	1.8	102	2	F87993	protein ZC334.3 [1
165	6	1.8	102	2	S72692	probable membrane
166	6	1.8	103	2	B97734	hypothetical prote
167	6	1.8	106	2	PH0987	Ig heavy chain V r
168	6	1.8	107	2	C70188	hypothetical prote
169	6	1.8	108	2	S73125	hypothetical prote
170	6	1.8	108	2	A55590	hypothetical prote
171	6	1.8	108	2	I40598	hypothetical prote
172	6	1.8	108	2	A54578	monocyte chemotact
173	6	1.8	109	2	H71142	hypothetical prote
174	6	1.8	109	2	G75009	hypothetical prote
175	6	1.8	111	2		
176	6	1.8	111	2	G64650	ribosome-binding f
177	6	1.8	111	2	F71940	probable ribosome-
178	6	1.8	111	2	B83101	hypothetical prote
179	6	1.8	112	2	S48472	probable membrane
180	6	1.8	112	2	S25266	T-cell receptor be
181	6	1.8	113	2	S17385	T-cell receptor be
182	6	1.8	113	2	S26262	T-cell receptor be
183	6	1.8	113	2	S26263	T-cell receptor be
184	6	1.8	113	2	UC4143	molt-inhibiting ho
185	6	1.8	113	2	AD2868	hypothetical prote
186	6	1.8	114	2	AC3023	hypothetical prote
187	6	1.8	115	2	AG3279	hypothetical prote
188	6	1.8	115	2	S09751	hypothetical prote
189	6	1.8	116	2	T51028	hypothetical prote
190	6	1.8	118	2	A97639	hypothetical prote
191	6	1.8	118	2	AB2862	conserved hypothet
192	6	1.8	118	2	H97644	hypothetical prote
193	6	1.8	120	2	I48147	monocyte chemotatr
194	6	1.8	122	2	A05304	hemoglobin beta-1
195	6	1.8	122	2	AB3283	hypothetical prote
196	6	1.8	123	2	E95940	conserved hypothet
197	6	1.8	123	2	I48192	surface antigen -
198	6	1.8	123	2	G75336	hypothetical prote
199	6	1.8	124	2	A11647	hypothetical prote
200	6	1.8	125	2	I46857	monocyte chemotatr
201	6	1.8	125	2	T27519	hypothetical prote
202	6	1.8	126	2	S73081	hypothetical prote
203	6	1.8	126	2	S30707	hypothetical 14.5K
204	6	1.8	126	2	AB0918	probable membrane
205	6	1.8	126	2	C72650	hypothetical prote
206	6	1.8	128	2	C48552	hypothetical prote
207	6	1.8	128	2	D29504	hypothetical 14K p
208	6	1.8	128	2	C75462	hypothetical prote
209	6	1.8	128	2	AD1386	hypothetical prote
210	6	1.8	128	2	AP1761	hypothetical prote
211	6	1.8	129	2	P95987	conserved hypothet
212	6	1.8	132	2	C87431	hypothetical prote
213	6	1.8	132	2	H75335	hypothetical prote
214	6	1.8	132	2	B83956	hypothetical prote
215	6	1.8	133	2	S57876	T cell receptor CK
216	6	1.8	133	2	C36886	hypothetical prote
217	6	1.8	134	2	D87021	probable DNA-bind
218	6	1.8	135	2	A70659	hypothetical prote
219	6	1.8	135	2	B83440	hypothetical prote
220	6	1.8	135	2	F87156	hypothetical prote
221	6	1.8	136	2	AD0630	probable exported
222	6	1.8	136	2	T22797	hypothetical prote
223	6	1.8	137	1	F64961	hypothetical prote
224	6	1.8	137	2	S03489	T-cell receptor be
225	6	1.8	137	2	C85815	hypothetical prote
226	6	1.8	137	2	D90967	hypothetical prote
227	6	1.8	137	2	A44031	probable membrane
228	6	1.8	139	2	S36296	T-cell receptor ga
229	6	1.8	140	2	C81176	hypothetical prote
230	6	1.8	140	2	A99253	hypothetical prote
231	6	1.8	141	2	E32998	chorion protein S1
232	6	1.8	141	2	D81309	probable acetyltra
233	6	1.8	142	2	T27965	hypothetical prote
234	6	1.8	143	2	D75617	response regulator
235	6	1.8	144	2	T27945	hypothetical prote
236	6	1.8	145	2	G82617	Virk protein Xf194
237	6	1.8	146	2	S26408	T-cell receptor be
238	6	1.8	146	2	T45385	ribosomal protein
239	6	1.8	146	2	T27964	hypothetical prote
240	6	1.8	149	2	AD3431	hypothetical prote
241	6	1.8	150	2	S43955	probable NADH2 de
242	6	1.8	150	2	A87714	hypothetical prote
243	6	1.8	151	2	S48958	hypothetical prote
244	6	1.8	151	2	A83784	acetyltransferase
245	6	1.8	152	2	S21826	T-cell receptor be
246	6	1.8	152	2	F86318	protein F15H18.2 (
247	6	1.8	153	1	A28406	gastric inhibitory
248	6	1.8	153	2	C64373	hypothetical prote

249	6	1.8	153	2	E87306	hypothetical prote	322	6	1.8	205	2	S42406	protein phosphatas
250	6	1.8	157	2	S57451	cysteine proteinas	323	6	1.8	205	2	S10497	hypothetical prote
251	6	1.8	157	2	T24917	hypothetical prote	324	6	1.8	206	2	AE0891	probable membrane
252	6	1.8	158	2	H96900	probable HD superf	325	6	1.8	206	2	S61705	hypothetical prote
253	6	1.8	159	2	D90586	hypothetical prote	326	6	1.8	206	2	AE2222	hypothetical prote
254	6	1.8	161	2	E72339	hypothetical prote	327	6	1.8	207	2	A35535	23k calcium-bindin
255	6	1.8	162	1	CFMKA	C-phycocyanin alph	328	6	1.8	209	2	H69552	hypothetical prote
256	6	1.8	162	1	CFMMA	C-phycocyanin alph	329	6	1.8	209	2	S69926	outer surface prot
257	6	1.8	162	1	S30940	phycocyanin alpha	330	6	1.8	209	2	T40285	outer surface prot
258	6	1.8	162	2	H72351	hypothetical prote	331	6	1.8	210	2	T50713	urease accessory p
259	6	1.8	163	2	A29674	phycocyanin alpha	332	6	1.8	210	2	G97037	hypothetical prote
260	6	1.8	163	2	AH1872	phycocyanin alpha	333	6	1.8	211	2	S69932	outer surface prot
261	6	1.8	165	2	G82910	peptide methionine	334	6	1.8	211	2	C59091	hypothetical prote
262	6	1.8	166	2	T11099	NADH2 dehydrogenas	335	6	1.8	212	2	B29010	alkylmercury lyase
263	6	1.8	170	2	T30570	NADH2 dehydrogenas	336	6	1.8	212	2	S69921	outer surface prot
264	6	1.8	171	2	E75662	hypothetical prote	337	6	1.8	212	2	S20543	outer surface prot
265	6	1.8	171	2	H87440	MutT/nudix family	338	6	1.8	212	2	S74247	outer surface prot
266	6	1.8	172	1	DEBTF6	hypothetical prote	339	6	1.8	213	2	S07573	CMP diacylglycerol
267	6	1.8	172	2	H72077	NADH2 dehydrogenas	340	6	1.8	213	2	C70346	amine oxidase (fla
268	6	1.8	172	2	C81590	conserved hypochet	341	6	1.8	214	1	S18729	UDP-N-acetoenolpyr
269	6	1.8	172	2	H86545	CT006 hypothetical	342	6	1.8	214	2	T21585	adenyllyl-sulfate k
270	6	1.8	174	2	T01466	hypothetical prote	343	6	1.8	215	2	G95170	hypothetical prote
271	6	1.8	176	2	S35949	edea protein - tre	344	6	1.8	215	2	G98036	hemolysin (importe
272	6	1.8	176	2	JC6152	orphanin FQ precur	345	6	1.8	215	2	T48789	conserved hypochet
273	6	1.8	177	2	S45364	ribosomal protein	346	6	1.8	216	2	H72277	TFPI related prote
274	6	1.8	177	2	B91248	hypothetical prote	347	6	1.8	216	2	T00192	hypothetical prote
275	6	1.8	178	2	S54190	hypothetical prote	348	6	1.8	217	2	S65830	alpha fucosidase p
276	6	1.8	179	2	S36295	outer surface prot	349	6	1.8	217	2	S49578	trypsin inhibitor
277	6	1.8	179	2	S54186	outer surface prot	350	6	1.8	217	2	H72390	dihydroorotate deh
278	6	1.8	179	2	S54187	outer surface prot	351	6	1.8	217	2	P91246	PTS system, sorbos
279	6	1.8	179	2	S54188	outer surface prot	352	6	1.8	218	2	B83862	endonuclease III (
280	6	1.8	179	2	T35439	probable integral	353	6	1.8	218	2	G64673	DNA polymerase III
281	6	1.8	180	2	S54189	outer surface prot	354	6	1.8	218	2	B71844	probable DNA pyme
282	6	1.8	180	2	S54191	outer surface prot	355	6	1.8	218	2	S74867	hypothetical prote
283	6	1.8	181	2	G89799	hypothetical prote	356	6	1.8	219	2	S49428	hypothetical prote
284	6	1.8	181	2	I40146	outer surface prot	357	6	1.8	221	1	S24328	glutathione peroxi
285	6	1.8	181	2	AC0686	hypothetical prote	358	6	1.8	221	2	A47367	24k androgen-depen
286	6	1.8	184	2	S73640	inorganic diphosph	359	6	1.8	221	2	B42719	O-methyltransferas
287	6	1.8	185	2	AG2026	hypothetical prote	360	6	1.8	222	2	JC7697	beta-casein-like p
288	6	1.8	186	1	HHF723	heat shock protein	361	6	1.8	222	2	AD2899	thiol:disulfide in
289	6	1.8	186	2	T11384	AtPase subunit 6 -	362	6	1.8	222	2	E98284	histone H1 - mouse
290	6	1.8	186	2	B20647	heat shock protein	363	6	1.8	223	2	S49492	conserved hypochet
291	6	1.8	187	2	T47804	hypothetical prote	364	6	1.8	224	2	F69444	hypothetical prote
292	6	1.8	187	2	G95076	conserved hypochet	365	6	1.8	225	2	G70721	hypothetical prote
293	6	1.8	187	2	H70450	lipoprotein nlpd h	366	6	1.8	227	2	F97276	CPSD/CAPA conserve
294	6	1.8	188	2	S50158	RER1 protein - yea	367	6	1.8	227	2	D84775	hypothetical prote
295	6	1.8	188	2	A69880	hypothetical prote	368	6	1.8	228	2	B90369	hypothetical prote
296	6	1.8	190	2	T33366	hypothetical prote	369	6	1.8	229	2	B90534	trna/rRNA methyltr
297	6	1.8	191	2	F82430	periplasmic nitrat	370	6	1.8	229	2	T18629	hypothetical prote
298	6	1.8	191	2	S70262	outer surface prot	371	6	1.8	230	2	D84215	hypothetical prote
299	6	1.8	192	2	S22981	T-cell surface gly	372	6	1.8	230	2	T36463	probable transcrip
300	6	1.8	192	2	UC4663	T-cell receptor CD	373	6	1.8	231	2	AF1798	probable N-acetyl
301	6	1.8	193	2	S70259	outer surface prot	374	6	1.8	232	2	B69392	ABC transporter, A
302	6	1.8	193	2	S70274	outer surface prot	375	6	1.8	233	2	B64925	trcbi protein - Hel
303	6	1.8	193	2	S70286	outer surface prot	376	6	1.8	235	2	S48924	hypothetical prote
304	6	1.8	194	2	D97944	conserved hypochet	377	6	1.8	235	2	D84961	oxoindole-5'-phosp
305	6	1.8	194	2	C83312	hypothetical prote	378	6	1.8	236	2	C75516	hypothetical prote
306	6	1.8	196	2	S54156	outer surface prot	379	6	1.8	236	2	E75337	hypothetical prote
307	6	1.8	197	2	E70642	probable ribosomal	380	6	1.8	237	2	S08073	cyclic nucleotide
308	6	1.8	197	2	G90671	hypothetical prote	381	6	1.8	237	2	S34727	listeriolysin regu
309	6	1.8	197	2	C85521	hypothetical prote	382	6	1.8	237	2	AH1424	a probable N-acety
310	6	1.8	197	2	B83768	hypothetical prote	383	6	1.8	237	2	T05249	hypothetical prote
311	6	1.8	200	2	E64756	membrane protein y	384	6	1.8	239	2	A81437	probable integral
312	6	1.8	200	2	A81295	conserved hypochet	385	6	1.8	239	2	T31881	hypothetical prote
313	6	1.8	201	2	D86912	conserved hypochet	386	6	1.8	240	2	AD1950	hypothetical prote
314	6	1.8	202	2	T110016	conserved hypochet	387	6	1.8	240	2	T47589	synaptobrevin-like
315	6	1.8	202	2	D69046	conserved hypochet	388	6	1.8	240	2	AG0048	hypothetical prote
316	6	1.8	202	2	B83375	hypothetical prote	389	6	1.8	241	2	T33804	hypothetical prote
317	6	1.8	203	2	AC0620	hypothetical proph	390	6	1.8	241	2	C86492	hypothetical prote
318	6	1.8	203	2	S32799	hypothetical prote	391	6	1.8	241	2	C72130	hypothetical prote
319	6	1.8	204	2	H70648	probable regulator	392	6	1.8	242	2	JC7517	casease-14/a - hum
320	6	1.8	204	2	B72370	hypothetical prote	393	6	1.8	243	2	G81255	1-(5-phosphoribosy
321	6	1.8	204	2	T51012	hypothetical prote	394	6	1.8	244	2	T43764	ATPase chain 6 [lm

395	6	1.8	245	2	D36145	precortin-2 methyl	468	6	1.8	276	2	A10565	lipoprotein [impor
396	6	1.8	245	2	B75340	transcription regu	469	6	1.8	276	2	E91117	hypothetical prote
397	6	1.8	245	2	F83105	hypothetical prote	470	6	1.8	276	2	F72342	conserved hypothet
398	6	1.8	246	2	T00704	hypothetical prote	471	6	1.8	276	2	T00923	hypothetical prote
399	6	1.8	247	2	A75254	conserved hypothet	472	6	1.8	276	2	U70591	Alu1 protein - yea
400	6	1.8	247	2	B86250	protein F25C20.16	473	6	1.8	277	2	T32460	hypothetical prote
401	6	1.8	247	2	D69064	conserved hypothet	474	6	1.8	277	2	B69479	conserved hypothet
402	6	1.8	248	2	D69094	phosphoribosylamin	475	6	1.8	278	1	TDRTOX	Ox-2 membrane glyc
403	6	1.8	249	2	S23902	genome polypeptid	476	6	1.8	279	2	E75472	ROK family protein
404	6	1.8	249	2	C75156	hypothetical prote	477	6	1.8	280	2	T02004	chitinase [EC 3.2.
405	6	1.8	250	2	H83213	hypothetical prote	478	6	1.8	280	2	B81100	2-dehydro-3-deoxy
406	6	1.8	250	2	T40977	cdp-diacylglycerol	479	6	1.8	280	2	G81840	2-dehydro-3-deoxy
407	6	1.8	250	2	E82821	NADH-ubiquinone ox	480	6	1.8	280	2	B45537	viral coat protein
408	6	1.8	251	2	C84036	succinate dehydrog	481	6	1.8	280	2	T32747	hypothetical prote
409	6	1.8	251	2	AC2187	phospho-2-dehydro-	482	6	1.8	280	2	B87547	transcription regu
410	6	1.8	251	2	B64851	flagellar basal bo	483	6	1.8	281	1	D69030	MJ1225-related pro
411	6	1.8	251	2	G90810	flagellar rod prot	484	6	1.8	281	1	B47092	copy control prote
412	6	1.8	251	2	C85670	flagellar rod prot	485	6	1.8	281	2	B86820	conserved hypothet
413	6	1.8	251	2	E72578	hypothetical prote	486	6	1.8	282	1	SAVL64	middle surface ant
414	6	1.8	252	2	H90212	enoyl CoA hydratase	487	6	1.8	282	2	AC3084	shikimate 5-dehydr
415	6	1.8	252	2	B47188	MHC class II histo	488	6	1.8	283	2	AH0726	phosphotransferase
416	6	1.8	253	2	S05029	H+-transporting tw	489	6	1.8	283	2	AC3340	maltoedextrin ABC-t
417	6	1.8	253	2	D88427	protein R07E5.15 l	490	6	1.8	283	2	A11710	maltoedextrin ABC-t
418	6	1.8	253	2	T30928	hypothetical prote	491	6	1.8	284	2	H64914	probable dimethylis
419	6	1.8	254	2	VCCVTV	coat protein - tob	492	6	1.8	284	2	H90915	probable DMSO redu
420	6	1.8	254	2	S25281	glfF protein precu	493	6	1.8	284	2	E85764	probable DMSO redu
421	6	1.8	255	2	F84244	proteasome, subun	494	6	1.8	284	2	C72222	UDP-N-acetylenolpy
422	6	1.8	256	2	T22715	hypothetical prote	495	6	1.8	284	2	T16934	probable transport
423	6	1.8	256	2	T00165	repressor - Staphy	496	6	1.8	285	2	E81388	probable succinate
424	6	1.8	257	2	B70246	outer surface prot	497	6	1.8	285	2	C98105	hypothetical prote
425	6	1.8	257	2	AC0087	probable flagellar	498	6	1.8	285	2	B95241	conserved hypothet
426	6	1.8	259	1	ONGAOL	ovulation hormone	499	6	1.8	286	1	WORCMM	phosphotransferase
427	6	1.8	260	2	I51544	MHC class II beta-	500	6	1.8	286	2	A98945	mannose-specific P
428	6	1.8	260	2	I51542	MHC class II beta-	501	6	1.8	286	2	D85793	PTS enzyme IID, ma
429	6	1.8	260	2	T33869	hypothetical prote	502	6	1.8	286	2	H64053	muirein endopeptida
430	6	1.8	260	2	T23909	hypothetical prote	503	6	1.8	287	1	A45168	probable 3-oxoacyl
431	6	1.8	260	2	S60480	low temperature-in	504	6	1.8	287	2	T04236	xyloglucan endo-1,
432	6	1.8	261	2	AE3499	O-sialoglycoprotei	505	6	1.8	288	2	S36956	cytochrome-c oxida
433	6	1.8	261	2	S10321	31k protein - frog	506	6	1.8	288	2	S28029	gene PD-1 protein
434	6	1.8	261	2	D95271	hypothetical prote	507	6	1.8	288	2	S18438	sporulation protei
435	6	1.8	262	1	OTPF3	cytochrome-c oxida	508	6	1.8	289	1	S25286	probable dehydroge
436	6	1.8	262	2	A81504	conserved hypothet	509	6	1.8	289	2	T41305	hypothetical prote
437	6	1.8	262	2	B72037	ct598 hypothetical	510	6	1.8	291	2	F98202	shikimate 5-dehydr
438	6	1.8	262	2	E86588	CT598 hypothetical	511	6	1.8	293	2	S04649	beta-Lactamase [EC
439	6	1.8	263	1	S23009	insulin-like growt	512	6	1.8	293	2	T09171	ribosomal protein
440	6	1.8	263	2	E72675	hypothetical prote	513	6	1.8	293	2	T09170	ribosomal protein
441	6	1.8	263	2	C69064	conserved hypothet	514	6	1.8	293	2	A83623	hypothetical prote
442	6	1.8	264	2	H81720	conserved hypothet	515	6	1.8	295	2	E84336	sugar kinase [limp
443	6	1.8	265	2	S16592	chlorophyll a/b-bi	516	6	1.8	295	2	AC0214	PTS system, mannos
444	6	1.8	265	2	F69742	hypothetical prote	517	6	1.8	296	2	T45930	uracil phosphoribo
445	6	1.8	267	2	A86891	hypothetical prote	518	6	1.8	296	2	T00559	hypothetical prote
446	6	1.8	267	2	H82301	probable bax prote	519	6	1.8	296	2	A36966	probable dTDP-rham
447	6	1.8	267	2	T29500	hypothetical prote	520	6	1.8	297	2	B91102	replication initia
448	6	1.8	267	2	C75131	hypothetical prote	521	6	1.8	297	2	F85947	replication initia
449	6	1.8	267	2	S70291	hypothetical prote	522	6	1.8	297	2	S22098	replication initia
450	6	1.8	268	2	A71086	hypothetical prote	523	6	1.8	297	2	AF0874	chromosome initia
451	6	1.8	269	2	A75397	probable signal pe	524	6	1.8	297	2	C96524	FLA147.4 [imported
452	6	1.8	269	2	I51539	MHC class II beta-	525	6	1.8	297	2	F70572	hypothetical prote
453	6	1.8	269	2	I51540	MHC class II beta-	526	6	1.8	297	2	A70347	UDP-N-acetylenolpy
454	6	1.8	269	2	S73959	hypothetical prote	527	6	1.8	298	2	T36900	probable integral
455	6	1.8	269	2	T04095	ribonuclease S hom	528	6	1.8	298	2	B35272	osteoinductive fac
456	6	1.8	269	2	H98273	iron(III) diclirat	529	6	1.8	298	2	T20841	hypothetical prote
457	6	1.8	270	2	I51543	MHC class II beta-	530	6	1.8	299	2	T04669	serine O-acetyltra
458	6	1.8	270	2	S57457	formylmethanofuran	531	6	1.8	299	2	AB0609	probable membrane
459	6	1.8	271	2	D83059	phosphatidylserine	532	6	1.8	299	2	T20953	hypothetical prote
460	6	1.8	272	2	H87075	probable conserved	533	6	1.8	300	2	A84220	proteolipase IV homo
461	6	1.8	273	2	B64446	formylmethanofuran	534	6	1.8	301	2	D90224	spermidine synthas
462	6	1.8	274	2	A47639	OX-2 membrane glyc	535	6	1.8	301	2	T37031	hypothetical prote
463	6	1.8	274	2	D97653	hypothetical prote	536	6	1.8	302	2	AE0112	chromosome initiat
464	6	1.8	274	2	AB2877	conserved hypothet	537	6	1.8	302	2	H87476	conserved hypothet
465	6	1.8	275	2	S74417	hypothetical prote	538	6	1.8	303	2	T30737	probable DNA-dirc
466	6	1.8	275	2	S03967	intercellular adhe	539	6	1.8	303	2	A10411	ferrichrome-bindin
467	6	1.8	276	1	PWYBAA	H+-transporting tw	540	6	1.8	303	2	S23440	hypothetical prote

541	6	1.8	304	2	T34271	614	6	1.8	338	2	AF3617	oligopeptide trans
542	6	1.8	304	2	A86614	615	6	1.8	338	2	T49998	hypothetical prote
543	6	1.8	304	2	T40316	616	6	1.8	339	2	S08981	malate dehydrog
544	6	1.8	304	2	E72010	617	6	1.8	339	2	S73840	ribonucleotide red
545	6	1.8	304	2	C81530	618	6	1.8	340	2	C64425	ribonucleotide red
546	6	1.8	305	2	JN0647	619	6	1.8	340	2	B96661	unknown protein, 8
547	6	1.8	305	2	T35344	620	6	1.8	340	2	T22010	hypothetical prote
548	6	1.8	305	2	AF2843	621	6	1.8	341	2	S55627	hypothetical prote
549	6	1.8	305	2	C97620	622	6	1.8	341	2	C90579	hypothetical prote
550	6	1.8	305	2	D88526	623	6	1.8	342	2	S53663	hydrogenase-relat
551	6	1.8	305	2	C84189	624	6	1.8	342	2	E90172	periplasmic protei
552	6	1.8	306	2	F83348	625	6	1.8	342	2	A85635	part of regulation
553	6	1.8	306	2	S77062	626	6	1.8	342	2	H64840	coat protein precu
554	6	1.8	307	2	B75120	627	6	1.8	343	2	A84335	chloromucinate cyc
555	6	1.8	307	2	E71011	628	6	1.8	343	2	AC3403	general L-amino ac
556	6	1.8	307	2	C81862	629	6	1.8	344	2	E84376	Na+/Ca2+-exchang
557	6	1.8	307	2	CRH082	630	6	1.8	344	2	T34981	probable integral
558	6	1.8	308	2	CRH06	631	6	1.8	345	2	S28140	gas vesicle protei
559	6	1.8	308	2	AG3317	632	6	1.8	345	2	A98251	hypothetical prote
560	6	1.8	309	2	H75113	633	6	1.8	345	2	AB3035	conserved hypochet
561	6	1.8	309	2	H89832	634	6	1.8	347	2	T11338	NADH2 dehydrogen
562	6	1.8	310	2	T40802	635	6	1.8	347	2	TL1481	NADH2 dehydrogen
563	6	1.8	311	2	S39661	636	6	1.8	347	2	B75610	probable 3-hydroxy
564	6	1.8	311	2	E95178	637	6	1.8	347	2	JC5788	tsec-1 protein (A
565	6	1.8	311	2	D98045	638	6	1.8	349	2	H95421	probable ABC trans
566	6	1.8	312	2	G84058	639	6	1.8	350	2	B82777	conserved hypochet
567	6	1.8	312	2	H89884	640	6	1.8	350	2	JC7188	REIC protein - hum
568	6	1.8	312	2	T09670	641	6	1.8	351	2	S25480	heat shock transcr
569	6	1.8	313	2	AB3186	642	6	1.8	351	2	JQ2166	spindle body prote
570	6	1.8	313	2	H84169	643	6	1.8	352	2	S24559	Wnt-2 protein - fr
571	6	1.8	313	2	T37901	644	6	1.8	352	2	T08209	matrix protein - H
572	6	1.8	315	2	JC5836	645	6	1.8	352	2	T49432	Ribonuclease III r
573	6	1.8	317	2	F82362	646	6	1.8	353	1	A45052	L-iditol 2-dehydro
574	6	1.8	317	2	B83039	647	6	1.8	353	2	A87643	hypothetical prote
575	6	1.8	317	2	D89361	648	6	1.8	354	2	C71368	probable UDP-N-ace
576	6	1.8	317	2	T21046	649	6	1.8	354	2	A90012	hypothetical prote
577	6	1.8	317	2	S44746	650	6	1.8	354	2	B47065	phosphate starvati
578	6	1.8	319	2	AB0324	651	6	1.8	354	2	B85647	hypothetical prote
579	6	1.8	323	2	A69648	652	6	1.8	354	2	B90787	ATP-binding pho re
580	6	1.8	324	2	B96606	653	6	1.8	354	2	T22274	hypothetical prote
581	6	1.8	324	2	PRMVA	654	6	1.8	355	1	S22181	gamma-1-microglobu
582	6	1.8	326	2	G70402	655	6	1.8	355	2	T03785	L-lactate dehydrog
583	6	1.8	327	2	A70871	656	6	1.8	356	2	C70249	hypothetical prote
584	6	1.8	328	2	D69452	657	6	1.8	356	2	S58529	alpha-complex prot
585	6	1.8	328	2	C69358	658	6	1.8	356	2	JQ2352	glycoprotein I - t
586	6	1.8	328	2	D72566	659	6	1.8	357	2	AD3491	hypothetical membr
587	6	1.8	328	2	T10203	660	6	1.8	357	2	D89823	hypothetical prote
588	6	1.8	329	2	H71192	661	6	1.8	358	2	H95892	probable oxidoredu
589	6	1.8	329	2	C71096	662	6	1.8	359	2	D83385	hypothetical prote
590	6	1.8	329	2	D95958	663	6	1.8	359	2	G86290	hypothetical prote
591	6	1.8	330	2	PS0079	664	6	1.8	359	2	AH3465	oxidoreductase (BC
592	6	1.8	330	2	D83480	665	6	1.8	360	2	T27694	hypothetical prote
593	6	1.8	330	2	T32158	666	6	1.8	360	2	B70863	hypothetical prote
594	6	1.8	331	2	T32445	667	6	1.8	360	2	T51870	hypothetical prote
595	6	1.8	331	2	MMBP26	668	6	1.8	361	2	SS7182	probable polygalac
596	6	1.8	332	2	AI1691	669	6	1.8	361	2	T31815	hypothetical prote
597	6	1.8	332	2	WMBP16	670	6	1.8	361	2	S29668	hypochetol prote
598	6	1.8	332	2	H82064	671	6	1.8	362	2	S78515	coat protein VPI -
599	6	1.8	333	2	B86567	672	6	1.8	362	2	A55525	single-stranded nu
600	6	1.8	333	2	D83750	673	6	1.8	363	2	AC0244	conserved hypochet
601	6	1.8	334	2	S44299	674	6	1.8	364	2	F96603	hypothetical prote
602	6	1.8	334	2	T27658	675	6	1.8	365	2	J00879	N55 protein - hepa
603	6	1.8	334	2	T27658	676	6	1.8	365	2	S42471	hnRNP protein E2 -
604	6	1.8	335	2	T27658	677	6	1.8	365	2	AI2940	acetyltransferase
605	6	1.8	335	2	T27658	678	6	1.8	366	2	E87457	conserved hypochet
606	6	1.8	335	2	T27658	679	6	1.8	366	2	A55525	carboxy-cis,cis-mu
607	6	1.8	336	2	T27658	680	6	1.8	366	2	T31933	hypothetical prote
608	6	1.8	336	2	T27658	681	6	1.8	367	2	B72644	probable transkeo
609	6	1.8	337	2	T27658	682	6	1.8	368	2	S71190	heat shock protein
610	6	1.8	337	2	T27658	683	6	1.8	368	2	AH2694	WFS permease (limpo
611	6	1.8	337	2	T27658	684	6	1.8	370	2	A60089	transforming prote
612	6	1.8	337	2	T27658	685	6	1.8	370	2	S29139	aggregran - pig (fr
613	6	1.8	337	2	T27658	686	6	1.8	370	2	G90248	conserved hypochet

687	6	1.8	371	2	A90044	hypothetical prote
688	6	1.8	371	2	A53908	brevican precursor
689	6	1.8	371	2	JC5498	G protein-coupled
690	6	1.8	371	2	G84358	N2,N2-dimethylguan
691	6	1.8	372	1	Q08588	glycoprotein I pre
692	6	1.8	372	1	PQ0138	dnak-type molecule
693	6	1.8	372	2	E84856	hypothetical prote
694	6	1.8	372	2	A98342	rspf protein (Af14
695	6	1.8	374	2	S40756	hypothetical prote
696	6	1.8	375	2	AH0209	probable sugar ABC
697	6	1.8	375	2	AI2041	hypothetical prote
698	6	1.8	376	2	AG1410	cell division prot
699	6	1.8	376	2	G83290	hypothetical prote
700	6	1.8	376	2	JC6535	multitubulin-cha

## ALIGNMENTS

## RESULT 1

H72621 hypothetical protein APE1433 - Aeropyrum pernix (strain KI)

C/Species: Aeropyrum pernix

C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999

C/Accession: H72621

R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A/Reference number: A72450; UID:99310339; PMID:10382966

A/Accession: H72621

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-156 &lt;KAW&gt;

A/Cross-references: DDBJ:AP000061; NID:95104821; PIDN:BA80430.1; PID:d1044216; PID:9510

A/Experimental source: strain KI

C/Genetics:

A:Gene: APE1433

Query Match	2.7%	Score 9;	DB 2;	Length 156;
Best Local Similarity	100.0%;	Pred. No. 0.45;		
Matches	9;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

Db 105 LTGSASGP 113

## RESULT 2

QRMSP1 microtubule-associated protein MAP1B - mouse

N/Alternate names: microtubule-associated protein MAP1 (X); microtubule-associated protei

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 01-Sep-2000

C/Accession: S07549; S44387; A33645

R/Noble, M.; Lewis, S.A.; Cowan, N.J.

J. Cell Biol. 109, 3367-3376, 1989

A/Title: The microtubule binding domain of microtubule-associated protein MAP1B contains

A/Reference number: A33645; UID:90094539; PMID:2480963

A/Accession: S07549

A/Molecule type: mRNA

A/Residues: 1-2464 &lt;NOB&gt;

A/Cross-references: EMBL:X51396; NID:952999; PIDN:CA35761.1; PID:953000

R/Sanchez, C.; Padilla, R.; Paciucci, R.; Zabalá, J.C.; Avila, J.

Arch. Biochem. Biophys. 310, 428-432, 1994

A/Title: Binding of heat-shock protein 70 (hsp70) to tubulin.

A/Reference number: S44387; UID:94234720; PMID:8179328

A/Accession: S44387

A/Status: preliminary

A/Molecule type: protein

A/Residues: 653-663, 'IC' &lt;SAN&gt;

C/Superfamily: microtubule-associated protein MAP1B

C/Keywords: microtubule binding; phosphoprotein; tandem repeat

F:589-786/Domain: microtubule binding #status experimental <MTB>  
 F:589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-690,691-69  
 R-K-E/D-X)  
 F:1861-2064/Region: 17-residue repeats  
 F:91,116,151,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: ph  
 F:147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (co  
 F:1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match	2.7%	Score 9;	DB 1;	Length 2464;
Best Local Similarity	100.0%;	Pred. No. 4.6;		
Matches	9;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

Db 812 AASGPVKEL 820

## RESULT 3

S76681 hypothetical protein - Synechocystis sp. (strain PCC 6803)

C/Species: Synechocystis sp.

A/Variety: PCC 6803

C/Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000

C/Accession: S76681

R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S.

A/Reference number: S74322; UID:97061201; PMID:8905231

A/Accession: S76681

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-173 &lt;KAN&gt;

A/Cross-references: EMBL:D64004; GB:AB001339; NID:91001701; PIDN:BA10625.1; PID:9120845

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Superfamily: cyanelle Cyanophora paradoxa hypothetical protein ycf36

Query Match	2.4%	Score 8;	DB 2;	Length 173;
Best Local Similarity	100.0%;	Pred. No. 4.9;		
Matches	8;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

Db 85 LILSLFVL 92

## RESULT 4

A82159 hypothetical protein VC1772 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C/Species: Vibrio cholerae

C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C/Accession: A82159

R/Heldberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathavan, J.; Bass, S.; Qin, H.; Dregoi, I.; Sellers, P

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A/Reference number: A82035; UID:20406833; PMID:10952301

A/Accession: A82159

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-286 &lt;HEI&gt;

A/Cross-references: GB:AB004254; GB:AB003852; NID:99656292; PIDN:AAF94921.1; GSPDB:GN001

A/Experimental source: serogroup O1; strain N16961; biotype El Tor

C/Genetics:

A:Gene: VC1772

A/Map position: 1

Query Match	2.4%	Score 8;	DB 2;	Length 286;
Best Local Similarity	100.0%;	Pred. No. 7.6;		
Matches	8;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY 261 EKKRVDIC 268  
 |||||  
 DB 134 EKKRVDIC 141

## RESULT 5

glutinin high molecular weight chain 189 precursor - wheat  
 C/Species: Triticum aestivum (common wheat)  
 C/Date: 08-Jun-1994 #sequence\_revision 10-Nov-1995 #text\_change 20-Aug-1999  
 C/Accession: S18733  
 R/Halford, N.G.; Forde, J.; Anderson, O.D.; Greene, F.C.; Shewry, P.R.  
 Theor. Appl. Genet. 75, 117-126, 1987  
 A/Title: The nucleotide and deduced amino acid sequences of an HMW glutenin subunit gene  
 A and 1D.  
 A/Reference number: S18733  
 A/Accession: S18733  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-705 <HML>  
 A/Cross-references: EMBL:X61026; NID:g22089; PIDN:CAA43361.1; PID:g22090  
 C/Superfamily: glutenin

Query Match 2.4%; Score 8; DB 2; Length 705;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 YSSSLOOP 115  
 |||||  
 DB 496 YSSSLOOP 503

## RESULT 6

desmoglein 2 - human  
 C/Species: Homo sapiens (man)  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Aug-1999  
 C/Accession: S38673; B38672  
 R/Zimbelmann, R.  
 Submitted to the EMBL Data Library, September 1993  
 A/Reference number: S38673  
 A/Accession: S38673  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-1117 <ZIM>  
 A/Cross-references: EMBL:Z26317; NID:g416177; PIDN:CAA81226.1; PID:g416178  
 R/Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.; Zimbelmann, R.; Franke, W.W.  
 Eur. J. Cell Biol. 55, 200-208, 1991  
 A/Title: Complete amino acid sequence of the epidermal desmoglein precursor polypeptide  
 A/Reference number: A38672; MUID:92037656; PMID:1935985  
 A/Accession: B38672  
 A/Molecule type: mRNA  
 A/Residues: 777-1117 <KOC>  
 A/Cross-references: GB:S64273  
 C/Genetics:  
 A/Gene: GDB:DSG2  
 A/Cross-references: GDB:128808; OMIM:125671  
 A/Map position: 18q12.1-18q12.2  
 C/Superfamily: cadherin; cadherin repeat homology  
 C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; membrane protein  
 F/51-158/Domain: cadherin repeat homology <CR1>  
 F/161-271/Domain: cadherin repeat homology <CR2>

Query Match 2.4%; Score 8; DB 2; Length 1117;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 LLLVPLLL 238  
 |||||  
 DB 624 LLLVPLLL 631

## RESULT 7

hypothetical protein ZC449.4 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
 C/Accession: T29918  
 R/Latrelle, P.; Gattung, S.  
 submitted to the EMBL Data Library, November 1995  
 A/Description: The sequence of C. elegans cosmid ZC449.  
 A/Reference number: Z20708  
 A/Accession: T29918  
 A/Molecule type: DNA  
 A/Residues: 1-105 <LAT>  
 A/Cross-references: EMBL:U41510; PIDN:AAA82633.1; CESP:ZC449.4  
 C/Genetics:  
 A/Gene: CESP:ZC449.4  
 A/Intons: 26/3; 51/1; 87/3  
 C/Superfamily: Caenorhabditis elegans hypothetical protein ZC449.4

Query Match 2.1%; Score 7; DB 2; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 MWLCLL 232  
 |||||  
 DB 63 MWLCLL 69

## RESULT 8

hypothetical protein jhp0956 - Helicobacter pylori (strain J99)  
 C/Species: Helicobacter pylori  
 A/Variety: strain J99  
 C/Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 04-Mar-2000  
 C/Accession: E71866  
 R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.  
 Nature 397, 176-180, 1999  
 A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path.  
 A/Reference number: A71800; MUID:99120557; PMID:9923682  
 A/Accession: E71866  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-161 <ARN>  
 A/Cross-references: GB:AE001525; GB:AE001439; NID:g4155533; PIDN:AAD06530.1; PID:g415553  
 A/Experimental source: strain J99  
 C/Genetics:  
 A/Gene: jhp0956  
 C/Superfamily: Helicobacter pylori hypothetical protein jhp0956

Query Match 2.1%; Score 7; DB 2; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 PULLSLF 241  
 |||||  
 DB 102 PULLSLF 108

## RESULT 9

hypothetical protein all0085 (imported) - Nostoc sp. (strain PCC 7120)  
 C/Species: Nostoc sp. PCC 7120  
 A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
 C/Accession: AE1817  
 R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamabe, S.; Watanabe, A.; Iritguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
 A/Reference number: AB1807; MUID:21595285; PMID:11759840  
 A/Accession: AE1817

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-170 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA077609.1; PID:gl7135063; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all0085

Query Match 2.1%; Score 7; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLICLUL 233  
|||||  
Db 14 VLICLUL 20

## RESULT 10

F97283  
ribosomal protein L6 [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 12-Jun-2003  
C:Accession: F97283  
R:Moiling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld

A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: F97283  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-179 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK01057.1; PID:gl5026184; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC3118  
C:Superfamily: ribosomal protein L6/L9

Query Match 2.1%; Score 7; DB 2; Length 179;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KELVGSV 33  
|||||  
Db 139 KELVGSV 145

## RESULT 11

F83305  
hypothetical protein PA2724 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: F83305  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: F83305  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-179 <STO>  
A:Cross-references: GB:AE004700; GB:AE004091; NID:g9948792; PIDN:AA060112.1; GSPDB:GN001

C:Genetics:  
A:Experimental source: strain PA01  
A:Gene: PA2724

Query Match 2.1%; Score 7; DB 2; Length 179;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 RVDPPDG 86

Db 42 RVDPPDG 48  
|||||

## RESULT 12

F97499  
hypothetical protein AGR\_C\_2123 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
C:Species: Agrobacterium tumefaciens  
C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C:Accession: F97499  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: F97499  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-182 <KUR>  
A:Cross-references: GB:AE007869; PIDN:AAK6951.1; PID:gl5156185; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR\_C\_2123  
A:Map position: circular chromosome

Query Match 2.1%; Score 7; DB 2; Length 182;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 LISLFLV 243  
|||||  
Db 34 LISLFLV 40

## RESULT 13

140220  
hypothetical protein 2 - Bacillus licheniformis (fragment)  
C:Species: Bacillus licheniformis  
C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 15-Oct-1999  
C:Accession: I40220  
R:Harry, J.T.; Partridge, S.R.; Weiss, A.S.; Wake, R.G.  
Gene 147, 85-89, 1994  
A>Title: Conservation of the 168 divB gene in Bacillus subtilis W23 and B. licheniformi

A:Reference number: I40220; MUID:94374713; PMID:8088553  
A:Accession: I40220  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-184 <RES>  
A:Cross-references: EMBL:U01958; NID:g404008; PIDN:AAA57244.1; PID:g404010

Query Match 2.1%; Score 7; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GSVGAV 37  
|||||  
Db 9 GSVGAV 15

## RESULT 14

H70416  
hypothetical protein aq\_1348 - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C>Date: 06-May-1998 #sequence\_revision 06-May-1998 #text\_change 24-Nov-1999  
C:Accession: H70416  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov  
V.  
Nature 392, 353-358, 1998  
A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: H70416  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-189 <AGF>



A/Cross-references: GB:AE000736; NID:g2983763; PIDN:AAC0734.1; PID:g2983775; GB:AE00065  
 A/Experimental source: strain VFS

C/Genetics:

A/Gene: aq\_1348

C/Superfamily: Aquifex aeolicus hypothetical protein aq\_1348

Query Match 2.1%; Score 7; DB 2; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 GLFLWFL 250  
 |||||  
 Db 142 GLFLWFL 148

# RESULT 15

T45543 hypothetical protein 2 [imported] - Klebsiella pneumoniae transposon Tn5711

C/Species: Klebsiella pneumoniae

C/Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 17-Mar-2000

C/Accession: T45543

R/Albiger, B.; Hubert, J.C.; Lett, M.C.  
 submitted to the EMBL Data Library, October 1998

A/Description: Composite transposons Tn5708 and Tn5709 are based on a Tn3-like element T

A/Reference number: 223003

A/Accession: T45543

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-199 <ALB>

A/Cross-references: EMBL:AF011907; PIDN:CAA09858.1

A/Experimental source: strain K11A

C/Genetics:

A/Mobile element: transposon Tn5711

C/Superfamily: Bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 2.1%; Score 7; DB 2; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 LLLSLFY 242  
 |||||  
 Db 132 LLLSLFY 138

Search completed: August 18, 2004, 16:17:04  
 Job time : 19 secs

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691	6	1.8	863	1	MCMA_XENLA	P30664 xenopus lae
692	6	1.8	870	1	CSX2_SCHPO	Q9uew2 schizosacch
693	6	1.8	870	1	Y563_HUMAN	O60309 homo sapien
694	6	1.8	874	1	SYA_F32AE	O91553 pseudomonas
695	6	1.8	877	1	PI01_PIG	O02696 sus scrofa
696	6	1.8	877	1	SECA_GUITH	Q78441 guillardia
697	6	1.8	880	1	BRCA_DROME	Q24206 drosophila
698	6	1.8	883	1	PGCB_MOUSE	O61361 mus musculu
699	6	1.8	883	1	PGCB_RAT	P55068 rattus norv
700	6	1.8	887	1	MCMA_DROME	P49735 drosophila

## ALIGNMENTS

RESULT 1  
MAPB\_MOUSE STANDARD; PRT; 2464 AA.

AC P14873;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))  
DE [Contains: MAP1 light chain LC1].  
GN MAP1B OR MTAP1B OR MTAP5.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND DOMAIN.  
RC STRAIN=Swiss Webster; TISSUE=Brain;  
RX MEDLINE=90094539; PubMed=2480963;  
RT Noble M., Lewis S.A., Cowan N.J.;  
RT "The microtubule binding domain of microtubule-associated protein  
MAPB contains a repeated sequence motif unrelated to that of MAP2  
and tau."  
RL J. Cell Biol. 109:3367-3376(1998).  
CC -|- FUNCTION: The function of brain MAPS is essentially unknown.  
CC Phosphorylated MAPB may play a role in the cytoskeletal changes  
CC that accompany neurite extension. Possibly MAPB binds to at least  
CC two tubulin subunits in the polymer, and this bridging of subunits  
CC might be involved in nucleating microtubule polymerization and in  
CC stabilizing microtubules.  
CC -|- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate  
CC with MAPB and MAPB proteins.  
CC -|- DOMAIN: Has a highly basic region with many copies of the sequence  
CC KKEE and KKEI/V, repeated but not at fixed intervals, which is  
CC responsible for the binding of MAPB to microtubules.  
CC -|- PTM: LC1 is coexpressed with MAPB. It is a polypeptide generated  
CC from MAPB by proteolytic processing. It is free to associate with  
CC both MAPA and MAPB. It interacts with the amino-terminal region  
CC of MAPB.  
CC -|- SIMILARITY: TO MAPA.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL, X51396; CAA5761.1; -.  
CC PIR, S07549; QRMSP1.  
CC MGD, MG1:1306778; Mtap1b.  
CC GO, GO:0016358; P.dendrite morphogenesis; IMP.  
CC GO, GO:0001578; P.microtubule bundling; IMP.  
CC InterPro: IPR000102; MAPB1.neuraxin.  
CC Pfam: PF00414; MAPB1.neuraxin; 10.  
CC PROSITE, PS00230; MAPB1.NEURAXIN; 7.  
CC Microtubule; Repeat; Phosphorylation.  
CC CHAIN ? 2464 MAP1 LIGHT CHAIN LC1.  
CC FT

FT	REPEAT	1874	1890	MAPB 1.
FT	REPEAT	1891	1907	MAPB 2.
FT	REPEAT	1908	1924	MAPB 3.
FT	REPEAT	1925	1941	MAPB 4.
FT	REPEAT	1942	1958	MAPB 5.
FT	REPEAT	1959	1975	MAPB 6.
FT	REPEAT	1993	2009	MAPB 7.
FT	REPEAT	2010	2026	MAPB 8.
FT	REPEAT	2027	2043	MAPB 9.
FT	REPEAT	2044	2060	MAPB 10.
FT	DOWIN	589	787	LTS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS).
FT	SEQUENCE	2464 AA;	270408 MW;	FBD3DD93CFD8A87 CRC64;

Query Match 2.7%; Score 9; DB 1; Length 2464;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 AASGPVKEL 29  
DB 812 AASGPVKEL 820

RESULT 2  
BGAL\_FELCA STANDARD; PRT; 669 AA.  
AC O19015; O18898;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid beta-  
DE galactosidase).  
GN GLB1 OR BGAL.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Varadarajan G.S., Smith B.F., Fourman P., Martin D.R.,  
RA Varadarajan U., Georgeson M., Baker H.J.;  
RT "The sequence of feline lysosomal beta-galactosidase."  
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Smith B.F., Fourman P., Georgeson M., Martin D.R., Baker H.J.;  
RT "The mutation in feline beta-galactosidase deficiency (GM1  
RT gangliosidosis)."  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
CC -|- FUNCTION: Cleaves beta-linked terminal galactosyl residues from  
CC gangliosides, glycoproteins, and glycosaminoglycans.  
CC -|- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-  
CC galactose residues in beta-D-galactosides.  
CC -|- SUBCELLULAR LOCATION: Lysosomal.  
CC -|- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL, AF006749; AAB81350.1; -.  
CC EMBL, AF029974; AAB86405.1; -.  
CC InterPro: IPR001944; Glyco\_hydro\_35.  
CC Pfam: PF01301; Glyco\_hydro\_35; 1.  
CC PRINTS: PR00742; GLHFDRLAS35.  
CC PROSITE, PS01182; GLYCOSYL\_HYDROL\_F35; 1.  
CC Hydrolase; Glycosidase; Lysosome; Signal; Glycoprotein.  
CC SIGNAL 1 24 POTENTIAL.  
CC FT



FT	PROPER	25	29	BY SIMILARITY.
FT	CHAIN	30	669	BETA-GALACTOSIDASE.
FT	ACT_SITE	189	189	PROTON DONOR (BY SIMILARITY).
FT	ACT_SITE	269	269	NUCLEOPHILE (POTENTIAL).
FT	CARBOHYD	27	27	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	248	248	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	465	465	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	499	499	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	547	547	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	557	557	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	483	483	R -> P (IN REF. 2).
SO	SEQUENCE	669 AA;	75229 MW;	35B84933BB5E2F76 CRC64;
Query Match	Best Local Similarity	2.4%;	Score 8;	DB 1; Length 669;
Matches	8; Conservative	100.0%;	Pred. No. 12;	Mismatches 0; Indels 0; Gaps 0;
Oy	231 LLLVPLLL 238			
Db	12 LLLVPLLL 19			
RESULT 3				
DSG2_HUMAN				
ID	_DSG2_HUMAN	STANDARD;	PRT;	1117 AA.
AC	Q1A1Z6;			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Desmoglein 2 precursor (HDGC).			
GN	DSG2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Colon carcinoma;			
RX	MEDLINE=94192736; PubMed=8143788;			
RA	Schaefer S., Koch P.J., Franke W.W.;			
RT	"Identification of the ubiquitous human desmoglein, Dsg2, and the			
RT	expression catalogue of the desmoglein subfamily of desmosomal			
RT	cadherins.";			
RL	Exp. Cell Res. 211:391-399(1994).			
RN	[2]			
RP	SEQUENCE OF 777-1117 FROM N.A.			
RX	MEDLINE=92037656; PubMed=1935985;			
RA	Koch P.J., Goldschmidt M.D., Walsh M.J., Zimbelmann R., Franke W.W.;			
RT	"Complete amino acid sequence of the epidermal desmoglein precursor			
RT	polypeptide and identification of a second type of desmoglein gene.";			
RL	Eur. J. Cell Biol. 55:200-208(1991).			
RP	[3]			
RP	CARBOHYDRATE-LINKAGE SITE ASN-111.			
RX	MEDLINE=22660472; PubMed=12754519.			
RA	Zhang H., Li X.-N., Martin D.B., Aebersold R.;			
RT	"Identification and quantification of N-linked glycoproteins using			
RT	hydrazide chemistry, stable isotope labeling and mass spectrometry.";			
RL	Nat. Biotechnol. 21:660-666(2003).			
CC	-1- FUNCTION: Component of intercellular desmosome junctions. Involved			
CC	in the interaction of plaque proteins and intermediate filaments			
CC	mediating cell-cell adhesion.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).			
CC	-1- TISSUE SPECIFICITY: All of the tissues tested and carcinomas.			
CC	-1- DOMAIN: Calcium may be bound by the cadherin-like repeats			
CC	(Potential).			
CC	-1- SIMILARITY: Contains 4 cadherin domains.			
CC	-----			
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CC	entities requires a license agreement (See <a href="http://www.isb-sb.ch/announce/">http://www.isb-sb.ch/announce/</a> )			

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CC EMBL, Z26317, CAA81226.1, -.
DR PIR, S38673, S38673.
DR HSSP, P15116, INCI.
DR Genew, HGNC:3049, DSG2.
DR MIM, 125671, -.
DR GO, GO:0005911, C:intercellular junction; TAS.
DR InterPro, IPR002126, Cadherin.
DR Pfam, PF00028, cadherin, 4.
DR PRINTS, PRO0205, CADHERIN.
DR SMART, SMO0112, CA, 4.
DR PROSITE, PS00232, CADHERIN_1, 3.
DR PROSITE, PS50268, CADHERIN_2, 4.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
KW Cytoskeleton; Calcium-binding.
FT SIGNAL 1 23
FT PROPEP 24 48
FT CHAIN 49 1117
FT DOMAIN 49 608
FT TRANSMEM 609 633
FT DOMAIN 634 1117
FT DOMAIN 49 159
FT DOMAIN 160 272
FT DOMAIN 273 387
FT DOMAIN 388 502
FT REPEAT 880 911
FT REPEAT 912 941
FT REPEAT 942 967
FT REPEAT 968 991
FT REPEAT 992 1020
FT REPEAT 1021 1050
FT CARBOHYD 111 111
FT CARBOHYD 181 181
FT CARBOHYD 308 308
FT CARBOHYD 461 461
FT CARBOHYD 513 513
SQ SEQUENCE 1117 AA, 122385 MW, 223897FE070B289 CRC64;

Query Match 2.4%; Score 8; DB 1; Length 1117;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 231 LLLVPLL 238
Db 624 LLLVPLL 631

RESULT 4
DSG2_MOUSE STANDARD; PRT; 1122 AA.
ID_DSG2_MOUSE
AC 055111, Q8K069, Q8R517;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Desmoglein 2 precursor.
DSG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Zhuxiang N., Garrard D. R.;
RT "Desmosomal cadherins mediate homophilic cell adhesion.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 348-1122 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257, PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,

```

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
RA Hopkin L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Staleron M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.T., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rahn S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Scherich A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[3]  
RP SEQUENCE OF 1042-1122 FROM N.A., AND TISSUE SPECIFICITY.  
RX MEDLINE=98067789; PubMed=9404003;  
RA King I.A., Angst B.D., Hunt D.M., Kruger M., Arremann J., Buxton R.S.,  
RT "Hierarchical expression of desmosomal cadherins during stratified  
RT epithelial morphogenesis in the mouse.";  
RL Differentiation 62:83-96(1997).  
CC -1- FUNCTION: Component of intercellular desmosome junctions. Involved  
CC in the interaction of plaque proteins and intermediate filaments  
CC mediating cell-cell adhesion.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -1- TISSUE SPECIFICITY: Expressed uniformly in all E12.5 epithelia,  
CC gradually becoming confined to the basal cell layers during  
CC epithelial stratification.  
CC -1- DOMAIN: Calcium may be bound by the cadherin-like repeats  
CC (Potential).  
CC -1- SIMILARITY: Contains 4 cadherin domains.  
CC -----  
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CC -----  
DR EMBL; AB072269; BAB86843.1; -;  
DR EMBL; BC034056; BAH34056.1; -;  
DR EMBL; AJ000328; CA03995.1; -;  
DR MGI; MGI:119646; Dsg2.  
DR GO; GO:003057; C:desmosome; IDA.  
DR InterPro; IPR002126; Cadherin.  
DR Pfam; PF00028; cadherin; 4.  
DR PRINTS; PR00205; CADHERIN.  
DR SMART; SM00112; CA; 4.  
DR PROSITE; PS00232; CADHERIN\_1; 3.  
DR PROSITE; PS50268; CADHERIN\_2; 4.  
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;  
KW Cytoskeleton; Calcium-binding.  
FT SIGNAL 1 28  
FT PROPEP 29 54  
FT CHAIN 55 1122  
FT DOMAIN 29 618  
FT TRANSMEM 619 639  
FT DOMAIN 640 1122  
FT DOMAIN 164 164  
FT DOMAIN 165 277  
FT DOMAIN 278 398  
FT DOMAIN 397 504  
FT REPEAT 885 916  
FT REPEAT 917 945  
FT REPEAT 946 971  
FT REPEAT 972 995  
FT REPEAT 996 1024  
FT REPEAT 1025 1055  
FT DESMOGLEIN REPEAT 5.  
FT DESMOGLEIN REPEAT 6.

FT CARHOVD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARHOVD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARHOVD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARHOVD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 358 358 I -> L (IN REF. 2).  
FT CONFLICT 480 480 E -> D (IN REF. 2).  
FT CONFLICT 491 491 V -> I (IN REF. 2).  
FT CONFLICT 863 863 T -> R (IN REF. 2).  
FT CONFLICT 899 899 R -> H (IN REF. 2).  
SQ SEQUENCE 1122 AA; 122397 MW; CEC0469F858ED57 CRC64;  
Query Match 2.4%; Score 8; DB 1; Length 1122;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 231 LLLVPLLL 238  
DB 630 LLLVPLLL 637  
RESULT 5  
MTRF\_METKA STANDARD; PRT; 75 AA.  
ID MTRF\_METKA  
AC Q8TVA7;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tetrahydromethanopterin S-methyltransferase subunit F (EC 2.1.1.86)  
DE (N5-methyltetrahydromethanopterin--coenzyme M methyltransferase  
DE subunit F).  
GN MTRF OR MK1485.  
OS Methanopyrus kandleri.  
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;  
OC Methanopyrus  
OX NCBI\_Taxid=2320;  
RM [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=AV19 / DSM 6324 / JCM 9639;  
RX MEDLINE=21927647; PubMed=11930014;  
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,  
RA Shecherintina O.V., Shakova V.V., Belova G.I., Aravind L.,  
RA Natelle D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,  
RA Mal'kh A.G., Koonin E.V., Kozlovskiy S.A.;  
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19  
RT and nonophily of archaeal methanogens";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).  
CC -1- FUNCTION: Part of a complex that catalyzes the formation of  
CC methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and  
CC methyl-tetrahydromethanopterin. This is an energy-conserving,  
CC sodium-ion translocating step (By similarity).  
CC -1- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-  
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-  
CC (methylthio)ethanesulfonate.  
CC -1- PATHWAY: Methanogenesis from carbon dioxide; sixth step.  
CC -1- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC,  
CC mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).  
CC -1- SUBCELLULAR LOCATION: Membrane-anchored (Potential).  
CC -1- MISCELLANEOUS: Unlike other orthologs, mtrF from M.kandleri is not  
CC located in the mtr operon.  
CC -1- SIMILARITY: Belongs to the mtrF family.  
CC -----  
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CC -----  
DR EMBL; AF010439; AAM02698.1; -;  
DR HAKAP; MF\_01099; -; 1.  
KW Methanogenesis; One-carbon metabolism; Transferase; Methyltransferase;  
KW Transmembrane; Complete proteome.

FT TRANSMEM 53 73 POTENTIAL.  
SQ SEQUENCE 75 AA; 8130 MW; 0186C402CCFCER28 CRC64;  
Query Match 2.1%; Score 7; DB 1; Length 75;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 LVLVLL 238  
DB 66 LVLVLL 72

RESULT 6  
SY08\_MOUSE STANDARD; PRT; 97 AA.  
AC 092121;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic protein 2) (MCP-2) (Monocyte chemoattractant protein 2).  
GN CCL8 OR SCYA8 OR MCP2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10990;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
RA Nonlyama H.;  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Yoshino M., Itoh M., Iehi Y., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Glisli C., King B., Kochiwa H., Ruelshann S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Maehio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barch G., Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F., Suzuki H., Togo-Oka K., Wang K.H., Wetz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S., Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
CC -1- FUNCTION: Chemotactic factor that attracts monocytes. This protein can bind heparin (By similarity).  
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.  
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CC -----  
DR EMBL: AB023418; BA75014.1; -  
DR EMBL: AK007842; BAB25365.1; -  
DR HSSP: P51671; IEOT.  
DR WGD: MG1:101878; Cc18.  
DR InterPro: IPR000827; CC\_chemokine\_sm1.  
DR InterPro: IPR001811; Chemokine\_IL8.

DR Pfam: PF00048; IL8; 1.  
DR SMART: SM00199; SCY; 1.  
DR PROSITE: PS00472; SMALL\_CYTOKINES\_CC; FALSE\_NEG.  
KW Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response.  
FT SIGNAL 1 19  
FT CHAIN 20 97  
FT DISULFID 32 57  
FT DISULFID 33 73  
SQ SEQUENCE 97 AA; 11017 MW; 65BB5722F2F98D54 CRC64;  
Query Match 2.1%; Score 7; DB 1; Length 97;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLCLLL 233  
DB 6 VLCLLL 12

RESULT 7  
SY13\_HUMAN STANDARD; PRT; 98 AA.  
AC 099616; O95689;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Small inducible cytokine A13 precursor (CCL13) (Monocyte chemotactic protein 4) (MCP-4) (Monocyte chemoattractant protein 4) (CX-beta-10) (MCP-1).  
GN CCL13 OR SCYA13 OR MCP4 OR NCCL1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
MEDLINE=97113354; PubMed=8955214;  
RA Garcia-Zepeda E.A., Combadieere C., Rothenberg M.E., Sarafi M.N., Lavigne F., Hamid Q., Murphy P.M., Luster A.D.;  
RT "Human monocyte chemoattractant protein (MCP)-4 is a novel CC chemokine with activities on monocytes, eosinophils, and basophils induced in allergic and nonallergic inflammation that signals through the CC chemokine receptors (CCR)-2 and -3."  
RL J. Immunol. 157:5613-5626(1996).  
[2]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 17-98.  
RC TISSUE=Fetal;  
MEDLINE=96235049; PubMed=8642349;  
RA Ugucioni M., Loetscher P., Forssmann U., Dewald B., Li H., Lima S.H., Li Y., Kreider B., Garotta G., Thelen M., Baggiolini M.;  
RT "Monocyte chemoattractant protein 4 (MCP-4), a novel structural and functional analogue of MCP-3 and eotaxin."  
RL J. Exp. Med. 183:2379-2384(1996).  
[3]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-33.  
RC TISSUE=Fetal;  
MEDLINE=9741179; PubMed=9195948;  
RA Berkout T.A., Sarau H.M., Moores K., White J.R., Elshourbagy N., Appelbaum E., Reape T.J., Bramer M., Makwana J., Foley J.J., Schmidt D.B., Imbruglia C., Macnulty D., Matthews J., O'Donnell K., O'Shannessy D., Scott M., Groc P.H.E., Macphie C.;  
RT "Cloning, in vitro expression, and functional characterization of a novel human CC chemokine of the monocyte chemotactic protein (MCP) family (MCP-4) that binds and signals through the CC chemokine receptor 2B."  
RL J. Biol. Chem. 272:16404-16413(1997).  
[4]  
RP SEQUENCE FROM N.A.  
RA Dante M., Gibson A.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
[5]  
RP SEQUENCE FROM N.A.

RC TISSUE=lung;  
RA Power C.A., Meyer A., Rison S.C.G., Guye-Coulin F., Wells T.N.C.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97213770; PubMed=9060459;  
RA Godtska R., Chantry D., Raport C.J., Schweickart V.L., Trong H.L.,  
RT Gray P.W.;  
RT "Monocytic chemotactic protein-4: tissue-specific expression and  
RT signaling through CC chemokine receptor-2";  
RL J. Leukoc. Biol. 61:353-360(1997).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Skin fibroblast;  
RL MEDLINE=99160888; PubMed=10049733;  
RA Hein H., Schluter C., Kulke R., Christophers E., Schroeder J.-M.,  
RT Bartels J.;  
RT "Genomic organization, sequence analysis and transcriptional  
RT regulation of the human MCP-4 chemokine gene (SCYA13) in dermal  
RT fibroblasts: a comparison to other eosinophilic beta-chemokines";  
RL Biochem. Biophys. Res. Commun. 255:470-476(1999).  
RN [8]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Brain;  
RL MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Iqbalpiano N.A., Peters G.J., Abramson R.D., Millhys S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek U.A., Gamarine P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP SEQUENCE OF 17-95 FROM N.A.  
RX TISSUE=ForeSkin;  
RA Bartels J.H., Schluter C., Richter E., Noso N., Christophers E.,  
RA Schroeder J.-M.;  
RT "Expression of a MCP-4 like novel CC-chemokine in human dermal  
RT fibroblasts: molecular cloning and RT-PCR analysis.";  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, lymphocytes,  
CC basophils and eosinophils, but not neutrophils. Signals through  
CC CCR2B and CCR3 receptors. Plays a role in the accumulation of  
CC leukocytes at both sides of allergic and nonallergic inflammation.  
CC May be involved in the recruitment of monocytes into the arterial  
CC wall during the disease process of atherosclerosis. May play a  
CC role in the monocyte attraction in tissues chronically exposed to  
CC exogenous pathogens.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Widely expressed. Found in small intestine,  
CC thymus, colon, lung, trachea, stomach and lymph node. Low levels  
CC seen in the pulmonary artery smooth muscle cells.  
CC -1- INDUCTION: By interleukin-1 and TNF-alpha.  
CC -1- PTM: ONE MAJOR ISOFORM MCP-4, AND TWO MINOR ISOFORMS (LA)MCP-4 AND  
CC (FNO)GALMCP-4 ARE PRODUCED BY DIFFERENTIAL SIGNAL CUEVAUGE.  
CC (LA)MCP-4 IS ABOUT 30 FOLD LESS ACTIVE THAN MCP-4.  
CC -1- MASS SPECTROMETRY: MW=9314; MW\_ERR=30; METHOD=MALDI; RANGE=17-98.  
CC -1- MASS SPECTROMETRY: MW=8760; MW\_ERR=30; METHOD=MALDI; RANGE=22-98.  
CC -1- MASS SPECTROMETRY: MW=8575; MW\_ERR=30; METHOD=MALDI; RANGE=24-98.  
CC -1- MISCELLANEOUS: This protein can bind heparin.

CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.  
CC -----  
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CC -----  
DR EMBL; U46767; AA38703.1; -;  
DR EMBL; AC002482; AAB6307.1; -;  
DR EMBL; X98306; CAA66950.1; -;  
DR EMBL; U59808; AAD09362.1; -;  
DR EMBL; AJ001634; CAA04888.1; -;  
DR EMBL; BC008621; AAH08621.1; -;  
DR EMBL; Z77650; CAB01111.1; -;  
DR HSSP; P51671; IEOT.  
DR Gene; HGNC:10611; CCL13.  
DR MIM; 601391; -;  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0008009; F:chemokine activity; TAS.  
DR GO; GO:0005102; F:receptor binding; TAS.  
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.  
DR GO; GO:0007267; P:cell-cell signaling; TAS.  
DR GO; GO:0006935; P:chemotaxis; TAS.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR000827; CC\_chemokine\_gml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR01721; FRACALKINE.  
DR SMART; SM00199; SCY\_1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
DR Cytokine; Chemotaxis; Signal; Glycoprotein; Inflammatory response;  
KW Pyrrolidone carboxylic acid.  
FT SIGNAL 1 16  
FT CHAIN 17 98  
FT CHAIN 24 98  
FT MOD\_RES 24 58  
FT DISULFD 34 58  
FT CARBOHD 35 29  
FT CONFLICT 93 98  
SQ SEQUENCE 98 AA; 10986 MW; 612688DFC308873 CR664;  
Query Match 2.1%; Score 7; DB 1; Length 98;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 227 VLICLL 233  
Db 6 VLICLL 12  
-----  
RESULT 8  
RLIX\_SPOFR  
ID RLIX\_SPOFR STANDARD; PRT; 177 AA.  
AC Q8WO17;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE 60S ribosomal protein L18a.  
GN RPL18A.  
OS Spodoptera frugiperda (Fall armyworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Amphiesmoptera; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Amphipyritinae; Spodoptera.  
OX NCBI\_TaxID=7108;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Landais I., Ogliastro M., Mita K., Nohata J., Lopez-Ferber M.,

RA Duonor-Cerutti M., Fournier P., Devauchelle G.;  
 RT "Full-length ribosomal protein sequence from an EST library of  
 RL Spodoptera frugiperda cells (Sf9).";  
 CC Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -----  
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 CC -----  
 CC EMBL: AY072289; AAL62470.1; -;  
 DR InterPro: IPR002670; Ribosomal\_L18ae.  
 DR Pfam: PF01775; Ribosomal\_L18ae; 1.  
 KW Ribosomal protein.  
 SQ SEQUENCE 177 AA; 20992 MW; 93D2F8517A5D0D14 CRC64;  
 Query Match 2.1%; Score 7; DB 1; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 32 SVSGAVT 38  
 DB 101 SVSGAVT 107  
 RESULT 9  
 MURB\_BACLI STANDARD; PRT; 184 AA.  
 ID MURB\_BACLI  
 AC Q45305;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE UDP-N-acetylglucosaminylglucosamine reductase (EC 1.1.1.158) (UDP-N-  
 DE acetylglucosamine dehydrogenase) (Fragment).  
 GN MURB  
 OS Bacillus licheniformis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1402;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5A2;  
 RX MEDLINE=94374713; PubMed=808553;  
 RA Harry E.J., Partidge S.R., Weiss A.S., Wake R.G.;  
 RT "Conservation of the 168 divB gene in Bacillus subtilis W23 and B.  
 RT licheniformis, and evidence for homology to ftsQ of Escherichia  
 RT coli";  
 RL Gene 147,85-89(1994).  
 CC -1- FUNCTION: Cell wall formation (By similarity).  
 CC -1- CATALYTIC ACTIVITY: UDP-N-acetylglucosamine + NADP(+) = UDP-N-  
 CC acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.  
 CC -1- COFACTOR: FAD.  
 CC -1- PATHWAY: Peptidoglycan biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
 CC -1- SIMILARITY: Belongs to the murB family.  
 CC -----  
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 CC -----  
 CC EMBL: U01958; AAA57244.1; -;  
 DR PIR: I40220; I40220.  
 DR HSSP: P08373; 2MBR.  
 DR HAMAP: MF\_00037; -; 1.  
 DR InterPro: IPR003170; MurB.  
 DR InterPro: IPR006094; Oxid\_FAD\_bind.  
 DR Pfam: PF01565; FAD\_binding\_4; 1.

DR Pfam: PF02873; MurB\_C; 1.  
 KW Peptidoglycan synthesis; Cell wall; Cell division; Oxidoreductase;  
 KM NADP; Flavoprotein; FAD.  
 FT NON\_TER  
 SQ SEQUENCE 184 AA; 20166 MW; 4114DB829AE21EFD CRC64;  
 Query Match 2.1%; Score 7; DB 1; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 31 GSVGAV 37  
 DB 9 GSVGAV 15  
 RESULT 10  
 YD48\_AQUAE STANDARD; PRT; 189 AA.  
 ID YD48\_AQUAE  
 AC Q67363;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein AQ\_1348.  
 GN AQ\_1348.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VF5;  
 RX MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Shead M.A., Keller M., Anjay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus";  
 RL Nature 392:353-358(1998).  
 CC -----  
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 CC -----  
 CC EMBL: AE000736; AAC0734.1; -;  
 DR PIR: H70416; H70416.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 189 AA; 21788 MW; A70F71A263221FBE CRC64;  
 Query Match 2.1%; Score 7; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 244 GLFLWFL 250  
 DB 142 GLFLWFL 148  
 RESULT 11  
 UT11\_ARATH STANDARD; PRT; 228 AA.  
 ID UT11\_ARATH  
 AC Q9M223;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Probable U3 small nuclear RNA-associated protein 11 (U3 snRNP-  
 DE associated protein 11).  
 GN AT3G60360 OR T8B10.20.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC euroids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016720; PubMed=11130713;  
 RA Salanoubat M., Lemcke K., Rieger M., Ansgorge W., Unsel M.,  
 RA Farman B., Valle G., Bioecker H., Perez-Alonso M., Obermaier B.,  
 RA Delenay M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,  
 RA De Simone V., Choise N., Artiguenave F., Robert C., Brotier P.,  
 RA Winkler P., Cattolico L., Weisenbach J., Saurin W., Quetier F.,  
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
 RA Wurmbach E., Dizonck H., Ertle H., Jordan N., Banger S.,  
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P.,  
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,  
 RA Conrad A., Hornischer K., Kauer G., Joehner T.-H., Nordstiel G.,  
 RA Reichelt U., Schafte M., Schoen O., Barges M., Terol J., Clement J.,  
 RA Navarro P., Collado C., Perez-Perez A., Olteneider B., Duchemin D.,  
 RA Cooke R., Laude M., Berger-Llauró C., Purnelle B., Masny D.,  
 RA de Haan M., Maere A.C., Alcaraz J.-P., Collet A., Caesuberta E.,  
 RA Monfort A., Argitau A., Flores M., Iqurri R., Vitale D.,  
 RA Manhandt G., Haase D., Schoff H., Rudd S., Zaccaria P., Mewes H.-W.,  
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
 RA Rooney T., Rizzo M., Wals A., Uteback T., Fujii C.Y., Shea T.P.,  
 RA Cressy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,  
 RA Pal G., Miltcher J., Sellers P., Gill J.E., Feldblum T.V.,  
 RA Prens D., Lin X., Nieman W.C., Salzberg S.L., White O., Ventur J.C.,  
 RA Frazer C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
 RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,  
 RA Kiyokawa S., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
 RT thaliana";  
 RT Nature 408:820-822(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=22954850; PubMed=14593172;  
 RA Yamada K., Lim J., Dale J.M., Chen H., Shim P., Palm C.J.,  
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,  
 RA Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari V.,  
 RA Arkawa T., Banh N., Banno F., Bowser L., Brooke S.Y., Cantucci P.,  
 RA Chao O., Choy N., Enju A., Goldsmith A.D., Gurjil M., Hansen N.P.,  
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,  
 RA Khan S., Koesema B., Ishida J., Jiang P.X., Jones T., Kawai J.,  
 RA Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
 RA Satou M., Tame R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,  
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RT "Empirical analysis of transcriptional activity in the Arabidopsis  
 RT genome";  
 RT Science 302:842-846(2003).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldman K.A.;  
 RT "Full-length cDNA from Arabidopsis thaliana";  
 RT Submitted (Mar-2002) to the EMBL/Genbank/DBD databases.  
 CC -i- FUNCTION: Involved in nucleolar processing of pre-18S ribosomal  
 CC RNA (By similarity).  
 CC -i- SUBUNIT: Component of the ribosomal small subunit (SSU)  
 CC processome (By similarity).  
 CC -i- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).  
 CC -i- SIMILARITY: Belongs to the UTP1 family.  
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 CC -----  
 DR EMBL; AL138646; CAB81823.1; -  
 DR EMBL; AY039876; AAK53980.1; -  
 DR EMBL; AY101514; AAM26635.1; -  
 DR EMBL; BT000725; AAN31867.1; -  
 DR EMBL; AY085156; AAM61709.1; -  
 DR PIR; T47847; T47847.  
 DR InterPro; IPR007144; Utp11.  
 DR Pfam; PF03998; Utp11; 1.  
 KW rRNA processing; Nuclear protein.  
 SQ SEQUENCE 228 AA; 27149 MW; DEDB3112383CB5A CRC64;  
 Qy 305 STEIRPK 311  
 Db 155 STEIRPK 161  
 RESULT 12  
 ID YTMW\_BACSU STANDARD; PRT; 239 AA.  
 AC 034315;  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Probable amino-acid ABC transporter permease protein ytmw.  
 GN YTMW\_OR BSU29360.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=96048467; PubMed=9387221;  
 RA Laplante A., Galleron N., Sorokin A., Ehrlich S.D.;  
 RT "Sequencing and functional annotation of the Bacillus subtilis genes  
 RT in the 200 kb rmb-dnaB region";  
 RT Microbiology 143:3431-3441(1997).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=96044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bortier M.G., Bessieres P., Bolyon A., Borchert S.,  
 RA Bortier R., Bortier L., Brans A., Braun M., Brigelli S.C., Bron S.,  
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denthoe F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Entian K.D., Ethington J., Fabre C., Ferrari E., Foulger D.,  
 RA Frit C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Gilm S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,  
 RA Guisepi G., Guy B.J., Haga K., Haele J., Harwood G.R., Henaut A.,  
 RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Jorin B., Karamata D., Kaashara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krohn S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Laber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Portolillo S., Prescott A.M.,  
 RA Presenc E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sektuchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni K.,  
 RA Toesto V., Uchiyama S., Vandenbol M., Vannier F., Vassartoli A.,  
 RA Viati A., Wambut R., Wedler E., Wedler H., Weltzner T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;  
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*  
 subsp. '1'".  
 RL Nature 390:249-256(1997).  
 CC -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT  
 CC SYSTEM YTMKLM FOR AN AMINO ACID. PROBABLY RESPONSIBLE FOR THE  
 CC TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport  
 CC system permease family. HisMo subfamily.  
 CC -----  
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 CC -----  
 DR EMBL: AF008220; AAC00327.1; -.  
 DR EMBL: Z99118; CAB14896.1; -.  
 DR PIR: F69996; F69996.  
 DR Subtilist; BG13886; YML.  
 DR InterPro: IPR000515; BPD transp.  
 DR Pfam: PF00528; BPD transp. 1.  
 DR PROSITE: PS0928; ABC\_TM1; 1.  
 KW Hypothetical protein; Transport; Amino-acid transport; Transmembrane;  
 KW Complete proteome.  
 FT TRANSMEM 25 45 POTENTIAL.  
 FT TRANSMEM 69 89 POTENTIAL.  
 FT TRANSMEM 96 116 POTENTIAL.  
 FT TRANSMEM 196 216 POTENTIAL.  
 SQ SEQUENCE 239 AA; 26239 MW; AE0D17AC254D6239 CRC64;  
 Query Match 2.1%; Score 7; DB 1; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 241 FVGLFL 247  
 DB 36 FVGLFL 42  
 RESULT 13  
 FLIP\_CAUCR :  
 ID FLIP\_CAUCR STANDARD; PRT; 266 AA.  
 AC Q45980;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Flagellar biosynthetic protein FlpP.  
 GN FLIP OR CC0951.  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;  
 OC Caulobacteraceae; Caulobacter.  
 OX NCBI\_TaxID=155892;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=95325304; PubMed=7601828;  
 RA Guber J.W., Boyd C.H., Jarvis M., Mangan E.K., Rizzo M.F.,  
 RA Wingrove J.A.;  
 RT "Temporal and spatial regulation of flpP, an early flagellar gene of  
 RT Caulobacter crescentus that is required for motility and normal cell  
 RT division.";  
 RL J. Bacteriol. 177:3656-3667(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=21173698; PubMed=11259647;  
 RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
 RA Kolonay J.F., Smit J., Craven M.B., Kouri H., Shetty J., Berry K.,  
 RA Ueberberg T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 RT "Complete genome sequence of *Caulobacter crescentus*.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 CC -1- FUNCTION: MAY BE A COMPONENT OF THE FLAGELLUM. IT IS REQUIRED FOR  
 CC NORMAL CELL DIVISION. MAY BE IMPLICATED IN THE SECRETION OF  
 CC VIRULENCE FACTORS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U20387; AAA66882.1; -.  
 DR EMBL: AE005772; AAK22935.1; -.  
 DR PIR: C87367; C87367.  
 DR TIGR: CC0951; -.  
 DR InterPro: IPR005837; FlpP.  
 DR InterPro: IPR005838; TypeIII\_P.  
 DR Pfam: PF00813; FlpP, 1.  
 DR PRINTS: PR01302; TYPEIIIPEPROT.  
 DR ProDom: PD002586; TypeIII\_P, 1.  
 DR TIGRFAMs: TIGR01103; flpP, 1.  
 DR PROSITE: PS01060; FLIP\_1; 1.  
 DR PROSITE: PS01061; FLIP\_2; 1.  
 KW Flagellum; Transmembrane; Complete proteome.  
 FT TRANSMEM 20 40 POTENTIAL.  
 FT TRANSMEM 58 78 POTENTIAL.  
 FT TRANSMEM 102 122 POTENTIAL.  
 FT TRANSMEM 202 222 POTENTIAL.  
 FT TRANSMEM 226 246 POTENTIAL.  
 SQ SEQUENCE 266 AA; 28527 MW; A84F17CB1C5A947 CRC64;  
 Query Match 2.1%; Score 7; DB 1; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 21 AASGPVK 27  
 DB 146 AASGPVK 152  
 RESULT 14  
 CFQX\_GUITH :  
 ID CFQX\_GUITH STANDARD; PRT; 293 AA.  
 AC Q78450;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CFQX protein homolog.  
 GN CFQX.  
 OS Guillardia theta (*Cryptomonas phi*).  
 OC Chloroplast.  
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.  
 OX NCBI\_TaxID=55529;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=99128221; PubMed=9929392;  
 RA Douglas S.B., Penny S.L.;  
 RT "The plastid genome of the cryptophyte alga, *Guillardia theta*:  
 RT complete sequence and conserved synteny groups confirm its common  
 RT ancestry with red algae.";  
 RL J. Mol. Evol. 48:236-244(1999).  
 CC -1- FUNCTION: Necessary for the expression of Rubisco (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Chloroplast.  
 CC -1- SIMILARITY: BELONGS TO THE CBX/CFQX FAMILY.

```

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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AF041468; AAC35641.1; -.
CC DR InterPro; IPR003593; AAA_ATPase.
CC DR InterPro; IPR003959; AAA_ATPase_cent.
CC DR Pfam; PF00004; AAA_1.
CC DR PRINTS; PR00819; CBXCFOXSUPER.
CC DR SMART; SM00382; AAA; 1.
CC DR ATP-binding; Chloroplast.
CC FT NP_BIND 72 79
CC FT SEQUENCE 293 AA; 33560 MW; 7F7476B7BC34915 CRC64;
CC
CC Query Match
CC Best Local Similarity 2.1%; Score 7; DB 1; Length 293;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
QY 60 LVTIOPE 66
DB 277 LVTIOPE 283

```

RESULT 15

```

ID MURB STRA3 STANDARD; PRT; 300 AA.
AC Q8E553; Q8D219;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetyleno[pyruvoyl]glucosamine reductase (EC 1.1.1.158) (UDP-N-
DE acetyl]muramate dehydrogenase).
GN MURB OR GBS1179 OR SAG1112.
OS Streptococcus agalactiae (serotype III), and
OC Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495; 216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaeser P., Ruenliok C., Buchrieser C., Chevalier F., Frangoul L.,
RA Msadek T., Zouine M., Couve E., Lalloui L., Poyart C., Trieu-Cuot P.,
RA Kunst P.;
RA "Genome sequence of Streptococcus agalactiae, a pathogen causing
RA invasive neonatal disease.",
RA Mol. Microbiol. 45:149-1513 (2002).
RA [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22223988; PubMed=12200547;
RA Tetelein H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.D., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kojanay J.F., Madupu R., Lewis M.R.,
RA Radune D., Pedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carey H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Bretoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rimando D., Rappunoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Frazer C.M.;
RA "Complete genome sequence and comparative genomic analysis of an
RA emerging human pathogen, serotype V Streptococcus agalactiae.",
RA Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
CC -!- FUNCTION: Cell wall formation (By similarity).
CC -!- CATALYTIC ACTIVITY: UDP-N-acetyl]muramate + NADP(+) = UDP-N-
CC acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.

```

```

CC -!- COFACTOR: FAD (By similarity).
CC -!- PATHWAY: Peptidoglycan biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the murB family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AL766849; CAD46838.1; -.
CC DR EMBL; AE014242; AAM99993.1; -.
CC DR SagsList; gbs1179; -.
CC DR TIGR; SAG1112; -.
CC DR HAMAP; MF_00037; -.
CC DR InterPro; IPR003170; MURB.
CC DR InterPro; IPR006094; Oxid_FAD_bind.
CC DR Pfam; PF01565; FAD binding_4; 1.
CC DR Pfam; PF02873; MurB_C; 1.
CC DR Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell division;
CC Peptidoglycan synthesis; Complete proteome.
CC KW Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell division;
CC Peptidoglycan synthesis; Complete proteome.
CC SEQUENCE 300 AA; 32978 MW; 3FC5590FBFED97 CRC64;
CC
CC Query Match
CC Best Local Similarity 2.1%; Score 7; DB 1; Length 300;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
QY 31 GSVGAV 37
DB 125 GSVGAV 131

```

Search completed: August 18, 2004, 16:15:46

Job time : 16 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:12:42 ; Search time 39 Seconds

(without alignments)  
2710.220 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 335  
Sequence: 1 MAGSPCTCLTLYILMQLTGS.....PHSLMLPDPRLPAYENVV 335

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

Database :

SPTRMBL.25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp Vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriopl.\*  
17: sp\_archaeopl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	335	100.0	335	4 Q9NQ25	Q9NQ25 homo sapien
2	257	76.7	296	4 Q8N6Y8	Q8N6Y8 homo sapien
3	257	76.7	328	4 Q9NY23	Q9NY23 homo sapien
4	234	69.9	335	4 Q9NY08	Q9NY08 homo sapien
5	210	62.7	228	4 Q8ND32	Q8ND32 homo sapien
6	156	2.7	156	17 Q9YCI8	Q9YCI8 aetopyrum p
7	9	2.7	294	11 Q91XA0	Q91XA0 mus musculu
8	9	2.7	300	11 Q8CJ63	Q8CJ63 mus musculu
9	9	2.7	333	11 Q8BHK6	Q8BHK6 mus musculu
10	9	2.7	335	11 Q8CJ65	Q8CJ65 mus musculu
11	9	2.7	335	11 Q8CJ64	Q8CJ64 mus musculu
12	9	2.7	335	11 Q8BTL2	Q8BTL2 mus musculu
13	8	2.4	83	16 Q884T6	Q884T6 pseudomonas
14	8	2.4	91	10 Q94E37	Q94E37 oryza sativ
15	8	2.4	129	4 Q8IVU0	Q8IVU0 homo sapien
16	8	2.4	173	16 Q55866	Q55866 synchocyst

17	8	2.4	202	16 Q7V2B6	Q7V2B6 prochloroco
18	8	2.4	211	2 Q95488	Q95488 prochloroco
19	8	2.4	286	16 Q9KR71	Q9KR71 vibrio chol
20	8	2.4	317	7 Q9TPE7	Q9TPE7 monodelphis
21	8	2.4	328	6 Q9BDP0	Q9BDP0 aotus trivi
22	8	2.4	347	7 Q9TPE7	Q9TPE7 monodelphis
23	8	2.4	348	16 Q7USC6	Q7USC6 rhodopirell
24	8	2.4	360	4 Q96S86	Q96S86 homo sapien
25	8	2.4	352	7 Q9TPE0	Q9TPE0 monodelphis
26	8	2.4	412	16 Q95RV6	Q95RV6 bradyrhizob
27	8	2.4	467	16 Q8D7P9	Q8D7P9 vibrio vuln
28	8	2.4	533	16 Q8KCC4	Q8KCC4 chlorobium
29	8	2.4	671	16 Q829E0	Q829E0 streptomyces
30	8	2.4	705	10 Q03871	Q03871 triticum ae
31	8	2.4	720	10 Q94T06	Q94T06 triticum ae
32	8	2.4	720	10 Q84T66	Q84T66 triticum tu
33	8	2.4	1053	5 Q9VH63	Q9VH63 diosophila
34	8	2.4	1053	5 Q9VH63	Q9VH63 diosophila
35	8	2.4	1235	4 Q95428	Q95428 homo sapien
36	8	2.4	66	11 Q9QWE3	Q9QWE3 mus sp. alp
37	7	2.1	75	17 Q8TVA7	Q8TVA7 methanopyru
38	7	2.1	90	6 Q9GK67	Q9GK67 oryctolagus
39	7	2.1	96	16 Q83E08	Q83E08 coxiella bu
40	7	2.1	97	6 Q9TFS6	Q9TFS6 bos taurus
41	7	2.1	97	11 Q9Z318	Q9Z318 cavia porce
42	7	2.1	101	16 Q82M02	Q82M02 streptomyces
43	7	2.1	105	5 Q23329	Q23329 caenorhabdi
44	7	2.1	115	2 Q8KX15	Q8KX15 synchococc
45	7	2.1	117	6 Q8HKK4	Q8HKK4 macaca fasc
46	7	2.1	120	5 Q9VMS7	Q9VMS7 diosophila
47	7	2.1	124	5 Q9BNJ9	Q9BNJ9 platydemus
48	7	2.1	126	6 Q9BR60	Q9BR60 macaca fasc
49	7	2.1	135	10 Q8GWH4	Q8GWH4 arabidopsis
50	7	2.1	143	4 Q86SP9	Q86SP9 homo sapien
51	7	2.1	145	17 Q8RY49	Q8RY49 mechanopyru
52	7	2.1	150	2 Q9REN9	Q9REN9 mycoplasma
53	7	2.1	153	2 Q9XK55	Q9XK55 klebsiella
54	7	2.1	156	12 Q9EM01	Q9EM01 amastrea moo
55	7	2.1	159	11 Q9D0N8	Q9D0N8 mus musculu
56	7	2.1	159	11 Q8BRC2	Q8BRC2 mus musculu
57	7	2.1	160	16 Q7TUK7	Q7TUK7 prochloroco
58	7	2.1	161	16 Q9ZKH9	Q9ZKH9 helicobacte
59	7	2.1	162	16 Q9EP38	Q9EP38 rhizobium 1
60	7	2.1	165	5 Q7YXD5	Q7YXD5 globodera r
61	7	2.1	165	16 Q98U36	Q98U36 rhizobium 1
62	7	2.1	167	2 Q46295	Q46295 clostridium
63	7	2.1	167	16 Q8XPC3	Q8XPC3 clostridium
64	7	2.1	169	8 Q94SJ6	Q94SJ6 zenopsis ne
65	7	2.1	170	16 Q85DK6	Q85DK6 anabaena sp
66	7	2.1	171	8 Q85DH2	Q85DH2 corydoras r
67	7	2.1	173	8 Q94YR3	Q94YR3 engraulis j
68	7	2.1	173	8 Q8HQLO	Q8HQLO amia calva
69	7	2.1	174	3 Q870Y3	Q870Y3 neurospora
70	7	2.1	174	8 Q8HL82	Q8HL82 synbranchus
71	7	2.1	175	8 Q9WJ45	Q9WJ45 talpa europ
72	7	2.1	175	8 Q7V8E4	Q7V8E4 mogera wogu
73	7	2.1	175	8 Q7V8D2	Q7V8D2 urotrichus
74	7	2.1	179	16 Q910B8	Q910B8 pseudomonas
75	7	2.1	179	16 Q97EJ3	Q97EJ3 clostridium
76	7	2.1	182	16 Q8Y365	Q8Y365 ralsentonia s
77	7	2.1	182	16 Q8UG92	Q8UG92 agrobacteri
78	7	2.1	183	13 Q8JH31	Q8JH31 gallus gall
79	7	2.1	185	15 Q7ZH80	Q7ZH80 human immun
80	7	2.1	185	15 Q7ZH77	Q7ZH77 human immun
81	7	2.1	186	11 Q80UC0	Q80UC0 mus musculu
82	7	2.1	187	16 Q9EUJ8	Q9EUJ8 salmoneilla
83	7	2.1	189	15 Q7ZH75	Q7ZH75 human immun
84	7	2.1	189	15 Q7ZH70	Q7ZH70 human immun
85	7	2.1	189	15 Q7ZH66	Q7ZH66 human immun
86	7	2.1	190	15 Q7ZH74	Q7ZH74 human immun
87	7	2.1	190	15 Q7ZH73	Q7ZH73 human immun
88	7	2.1	190	15 Q7ZH72	Q7ZH72 human immun
89	7	2.1	190	15 Q7ZH71	Q7ZH71 human immun









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674 6 1.8 135 16 Q7TVC5 Q7EVC5 mycobacteri
675 6 1.8 136 5 Q45582 Q45582 caenorhabd
676 6 1.8 136 5 Q9XYH8 Q9XYH8 leishmani
677 6 1.8 136 6 Q8WRA0 Q8WRA0 cynocephalu
678 6 1.8 136 11 Q9CQK5 Q9CQK5 mus musculu
679 6 1.8 136 13 Q9DDX3 Q9DDX3 xenopus lae
680 6 1.8 137 5 Q9B129 Q9B129 chlamys isl
681 6 1.8 137 12 Q9E2N0 Q9E2N0 hepatitis c
682 6 1.8 137 16 Q8CVY5 Q8CVY5 escherichia
683 6 1.8 137 16 Q88MD0 Q88MD0 pseudomonas
684 6 1.8 137 16 Q83KM3 Q83KM3 shigella fl
685 6 1.8 138 2 Q93K18 Q93K18 uncultured
686 6 1.8 138 12 Q91CE6 Q91CE6 west nile v
687 6 1.8 138 12 Q77YN4 Q77YN4 bubaline he
688 6 1.8 138 13 Q9DDY2 Q9DDY2 xenopus lae
689 6 1.8 138 17 Q8Z2A5 Q8Z2A5 pyrobaculum
690 6 1.8 139 2 Q99068 Q99068 uncultured
691 6 1.8 139 2 Q9AF44 Q9AF44 uncultured
692 6 1.8 139 2 Q9AF45 Q9AF45 uncultured
693 6 1.8 139 2 Q9AF46 Q9AF46 uncultured
694 6 1.8 139 5 Q9BNG1 Q9BNG1 carcinoscor
695 6 1.8 139 5 Q9BNF2 Q9BNF2 chthonius t
696 6 1.8 139 16 Q89S26 Q89S26 bradyrhizob
697 6 1.8 139 16 Q88F26 Q88F26 pseudomonas
698 6 1.8 140 3 Q92276 Q92276 saccharomyc
699 6 1.8 140 16 Q9KOF8 Q9KOF8 neisseria m
700 6 1.8 140 16 Q8U957 Q8U957 agrobacteri

```

## ALIGNMENTS

## RESULT 1

```

ID Q9NQ25 PRELIMINARY; PRT; 335 AA.
AC Q9NQ25;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BA04P10.4 (Novel lty9 (lymphocyte antigen 9) like protein) (NK cell
DE receptor) (Membrane protein FOAP-12) (CD2-like receptor activating
DE cytotoxic cells) .
OS BA04P10.4 OR CSI.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bates K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Boles K.S., Mathew P.A. Sr.;
RL "Cloning of a new member of the CD2 subset of receptors expressed on
RL NK cells."
RN Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RA Fujii Y., Takayama K., Tsuritani K., Yajima Y., Amemiya T., Ukai Y.,
RA Naito K., Kawaguchi A.;
RL "Homo sapiens mRNA for FOAP-12 protein, complete cds."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;
RL "Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a SAP-
RL Independent Receptor of the CD2 Family."
RL J. Immunol. 167:0-0(2001) .
DR EMBL; AL121985; CAC00579.1; -
DR EMBL; AF291815; AAK11549.1; -
DR EMBL; AB027233; BAB61022.1; -

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DR EMBL; AF390894; AAL26989.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 335 AA; 37421 MW; D09ABBCF74BE8D4 CRC64;

```

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Query Match 100.0%; Score 335; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAGSPTCLTLIYIIMQLTGSAAAGPVKELVSGVGAVTFPLSKKKQVDSIYMTNTTPL 60
DB 1 MAGSPTCLTLIYIIMQLTGSAAAGPVKELVSGVGAVTFPLSKKKQVDSIYMTNTTPL 60
QY 61 VTIOPEGGTTIVTQNRNERVDPPDGYSLKLSKLNKDSGIYVGIYSSSIQOPSTOBY 120
DB 61 VTIOPEGGTTIVTQNRNERVDPPDGYSLKLSKLNKDSGIYVGIYSSSIQOPSTOBY 120
QY 121 VLAHYEHLSPKRVMTGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALQOANESHNGSIL 180
DB 121 VLAHYEHLSPKRVMTGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALQOANESHNGSIL 180
QY 181 PISRWGSDMTFICVARNPVSRNFSPIILARKLCEGAADPDSSMVLCLLVLPLLSL 240
DB 181 PISRWGSDMTFICVARNPVSRNFSPIILARKLCEGAADPDSSMVLCLLVLPLLSL 240
QY 241 FVLGLFPLFKREROEYIEKKRVDICRETPNICPHSGENTYDTIPIHNTFTIKEDPA 300
DB 241 FVLGLFPLFKREROEYIEKKRVDICRETPNICPHSGENTYDTIPIHNTFTIKEDPA 300
QY 301 NTVYSTVEIPKKMHPHSLTMPDPRFLPAYENV 335
DB 301 NTVYSTVEIPKKMHPHSLTMPDPRFLPAYENV 335

```

## RESULT 2

```

ID Q8N6Y8 PRELIMINARY; PRT; 296 AA.
AC Q8N6Y8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 19A24 protein.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC027867; AAH27867.1; -.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 296 AA; 32561 MW; B85D277192494EEC CRC64;

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Query Match 76.7%; Score 257; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 5e-259;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAGSPTCLTLIYIIMQLTGSAAAGPVKELVSGVGAVTFPLSKKKQVDSIYMTNTTPL 60
DB 1 MAGSPTCLTLIYIIMQLTGSAAAGPVKELVSGVGAVTFPLSKKKQVDSIYMTNTTPL 60
QY 61 VTIOPEGGTTIVTQNRNERVDPPDGYSLKLSKLNKDSGIYVGIYSSSIQOPSTOBY 120
DB 61 VTIOPEGGTTIVTQNRNERVDPPDGYSLKLSKLNKDSGIYVGIYSSSIQOPSTOBY 120
QY 121 VLAHYEHLSPKRVMTGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALQOANESHNGSIL 180

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Db      121 VLHVEHLSPKVTMLGQSNKNGTCVTNLTCCMEHGEEDVITYTWKALGQANSHNGSIL 180
QY      181 PISWRGSESDMTFICVARNPVSRNFSSPILARKLCEGAADPPSSWVLLCLLVPLLLSL 240
Db      181 PISWRGSESDMTFICVARNPVSRNFSSPILARKLCEGAADPPSSWVLLCLLVPLLLSL 240
QY      241 FVLGLFLMFLKRREROE 257
Db      241 FVLGLFLMFLKRREROE 257

RESULT 3
Q9NY23 PRELIMINARY; PRT; 328 AA.
AC Q9NY23;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 19A24 protein.
GN 19A24.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT "An early response gene that encodes an immunoglobulin superfamily
RT member with structural similarity to CD2."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: A2727869; CAB76561.1; -.
DR InterPro: IPR003599; IG.
DR SMART; SMART0409; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 328 AA; 36490 MW; E68A7243964380DB CRC64;

Query Match 76.7%; Score 257; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.5e-259;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILMQLTGSAAAGPVKEIVSGAVTFPLSKVKQVDSIVWTFNTTTL 60
Db 1 MAGSPCTCLTIYILMQLTGSAAAGPVKEIVSGAVTFPLSKVKQVDSIVWTFNTTTL 60
QY 61 VTIQPEGGTIIYVQNNRRERVDPPDGYSILSKLKKNDGSIYVGVYSSSLQOPESTOEY 120
Db 61 VTIQPEGGTIIYVQNNRRERVDPPDGYSILSKLKKNDGSIYVGVYSSSLQOPESTOEY 120
QY 121 VLHVEHLSPKVTMLGQSNKNGTCVTNLTCCMEHGEEDVITYTWKALGQANSHNGSIL 180
Db 121 VLHVEHLSPKVTMLGQSNKNGTCVTNLTCCMEHGEEDVITYTWKALGQANSHNGSIL 180
QY 181 PISWRGSESDMTFICVARNPVSRNFSSPILARKLCEGAADPPSSWVLLCLLVPLLLSL 240
Db 181 PISWRGSESDMTFICVARNPVSRNFSSPILARKLCEGAADPPSSWVLLCLLVPLLLSL 240
QY 241 FVLGLFLMFLKRREROE 257
Db 241 FVLGLFLMFLKRREROE 257

RESULT 4
Q9NY08 PRELIMINARY; PRT; 335 AA.
AC Q9NY08;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 19A protein.
GN 19A.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT "An early response gene that encodes an immunoglobulin superfamily
RT member with structural similarity to CD2."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: A276429; CAB81950.2; -.
DR InterPro: IPR003599; IG.
DR SMART; SMART0409; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 335 AA; 37403 MW; BB758B505CA4DD5 CRC64;

Query Match 69.9%; Score 234; DB 4; Length 335;
Best Local Similarity 99.7%; Pred. No. 5.4e-235;
Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILMQLTGSAAAGPVKEIVSGAVTFPLSKVKQVDSIVWTFNTTTL 60
Db 1 MAGSPCTCLTIYILMQLTGSAAAGPVKEIVSGAVTFPLSKVKQVDSIVWTFNTTTL 60
QY 61 VTIQPEGGTIIYVQNNRRERVDPPDGYSILSKLKKNDGSIYVGVYSSSLQOPESTOEY 120
Db 61 VTIQPEGGTIIYVQNNRRERVDPPDGYSILSKLKKNDGSIYVGVYSSSLQOPESTOEY 120
QY 121 VLHVEHLSPKVTMLGQSNKNGTCVTNLTCCMEHGEEDVITYTWKALGQANSHNGSIL 180
Db 121 VLHVEHLSPKVTMLGQSNKNGTCVTNLTCCMEHGEEDVITYTWKALGQANSHNGSIL 180
QY 181 PISWRGSESDMTFICVARNPVSRNFSSPILARKLCEGAADPPSSWVLLCLLVPLLLSL 240
Db 181 PISWRGSESDMTFICVARNPVSRNFSSPILARKLCEGAADPPSSWVLLCLLVPLLLSL 240
QY 241 FVLGLFLMFLKRREROEYIEKKRVVICRETPNIGHSEENETDPTPTNRTILKEDPA 300
Db 241 FVLGLFLMFLKRREROEYIEKKRVVICRETPNIGHSEENETDPTPTNRTILKEDPA 300
QY 301 NTYVSTVEIIPKQENPHSLTMDPTPLPAYENV 335
Db 301 NTYVSTVEIIPKQENPHSLTMDPTPLPAYENV 335

RESULT 5
Q8ND32 PRELIMINARY; PRT; 228 AA.
AC Q8ND32;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP667F126.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RA Bioecker H., Boecker M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL834424; CAD39085.1; -.
DR InterPro: IPR007110; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Hypothetical protein.
SQ SEQUENCE 228 AA; 25831 MW; 2B01DB70E7BBFC14 CRC64;

Query Match 62.7%; Score 210; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4e-210;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 126 EHLSPKVTMGLOSNKNGTCVTNLTCCMEHGEDVITYTWKALGOANESHNGSILPISWR 185
DB 19 EHLSPKVTMGLOSNKNGTCVTNLTCCMEHGEDVITYTWKALGOANESHNGSILPISWR 78
QY 186 WBSMDMTFCVARNPNVSRNPFSSPILARKLCEGAADPDSSMWLLCLLVPLLSLFLVGL 245
DB 79 WBSMDMTFCVARNPNVSRNPFSSPILARKLCEGAADPDSSMWLLCLLVPLLSLFLVGL 138
QY 246 FLMFLKREOROEYIEKKRVDICRETPNICPSGENTEXTDTPHTNRTILKEDPANTVYS 305
DB 139 FLMFLKREOROEYIEKKRVDICRETPNICPSGENTEXTDTPHTNRTILKEDPANTVYS 198
QY 306 TVEIPKMEKPNHSLTMDPTPLFAFAYENYI 335
DB 199 TVEIPKMEKPNHSLTMDPTPLFAFAYENYI 228

RESULT 6
QYCY18 PRELIMINARY; PRT; 156 AA.
AC Q9YCI8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE Hypothetical protein APE1433.
GN APE1433.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1.
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Koeugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
DR EMBL; AF000061; BAA80430.1; -.
DR PIR; H72621; H72621.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 156 AA; 15954 MW; 73BBB5C9FBE453D CRC64;

Query Match 2.7%; Score 9; DB 17; Length 156;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LTGSAASGP 25
DB 105 LTGSAASGP 113

RESULT 7
QY1XAO PRELIMINARY; PRT; 294 AA.
AC Q91XAO;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to 19A24 protein.
GN 4930560D03R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354683; PubMed=12466851;
```

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RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011154; AA011154.1; -.
DR MGD; MGI:1922595; 4930560D03R1K.
DR InterPro; IPR007110; IG-1-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 294 AA; 32782 MW; F4C8B8C4CFMA1AFB CRC64;

Query Match 2.7%; Score 9; DB 11; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 OSNKNKTCV 146
DB 135 OSNKNKTCV 143

RESULT 8
Q8CJ63 PRELIMINARY; PRT; 300 AA.
AC Q8CJ63;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Leukocyte cell-surface antigen isoform 8.
GN 4930560D03R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Thymus;
RX MEDLINE=22226696; PubMed=12242590;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA Bosch V., Terhorst C., Engel P.,
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors."
RL Immunogenetics 54:394-402(2002).
DR EMBL; AF467911; AA061160.1; -.
DR PIR; P70566; P70566.
DR MGD; MGI:1922595; 4930560D03R1K.
DR InterPro; IPR007110; IG-1-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 300 AA; 33332 MW; 9948108710BBBC3D CRC64;

Query Match 2.7%; Score 9; DB 11; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 OSNKNKTCV 146
DB 135 OSNKNKTCV 143

RESULT 9
Q8BHK5 PRELIMINARY; PRT; 333 AA.
AC Q8BHK5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to 19A24 protein homolog.
GN 4930560D03R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Aorta;
RX MEDLINE=22354683; PubMed=12466851;
```



RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
DR EMBL; AK030135; BAC26801.1; -.  
DR EMBL; AK030148; BAC26810.1; -.  
DR EMBL; AK040678; BAC30665.1; -.  
DR PIR; PT0566; PT0566.  
DR MGD; MGI:1922595; 4930560D03Rik.  
DR InterPro; IPR007110; IG-like.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
SQ SEQUENCE 333 AA; 37217 MW; 0CC9A0AAFEACD46E CRC64;  
  
Query Match 2.7%; Score 9; DB 11; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 138 QSNKNGTCV 146  
DB 135 QSNKNGTCV 143  
  
RESULT 10.  
Q8CJ65 PRELIMINARY; PRT; 335 AA.  
ID Q8CJ65;  
AC Q8CJ65;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DE Leukocyte cell-surface antigen.  
GN 4930560D03Rik.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=22226696; PubMed=12242590;  
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,  
RT Bosch J., Terhorst C., Engel P.;  
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of  
RT leukocyte cell-surface receptors."  
RL Immunogenetics 54:394-402(2002).  
DR EMBL; AF467909; AAN63158.1; -.  
DR PIR; PT0566; PT0566.  
DR MGD; MGI:1922595; 4930560D03Rik.  
DR InterPro; IPR007110; IG-like.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
SQ SEQUENCE 335 AA; 37493 MW; C210B9CEADCE8F3EB CRC64;  
  
Query Match 2.7%; Score 9; DB 11; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 138 QSNKNGTCV 146  
DB 135 QSNKNGTCV 143  
  
RESULT 11  
Q8CJ64 PRELIMINARY; PRT; 335 AA.  
ID Q8CJ64;  
AC Q8CJ64;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Leukocyte cell-surface antigen.  
GN 4930560D03Rik.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Thymus;  
RX MEDLINE=22226696; PubMed=12242590;  
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,  
RT Bosch J., Terhorst C., Engel P.;  
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of  
RT leukocyte cell-surface receptors."  
RL Immunogenetics 54:394-402(2002).  
DR EMBL; AF467910; AAN63159.1; -.  
DR PIR; PT0566; PT0566.  
DR MGD; MGI:1922595; 4930560D03Rik.  
DR InterPro; IPR007110; IG-like.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
SQ SEQUENCE 335 AA; 37590 MW; 85F00ABDFC8B90A0 CRC64;  
  
Query Match 2.7%; Score 9; DB 11; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 138 QSNKNGTCV 146  
DB 135 QSNKNGTCV 143  
  
RESULT 12  
Q8BT12 PRELIMINARY; PRT; 335 AA.  
ID Q8BT12;  
AC Q8BT12;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Similar to 19A24 protein homolog.  
GN 4930560D03Rik.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
DR EMBL; AK089525; BAC40914.1; -.  
DR PIR; PT0566; PT0566.  
DR MGD; MGI:1922595; 4930560D03Rik.  
DR InterPro; IPR007110; IG-like.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
SQ SEQUENCE 335 AA; 37521 MW; 99E802E55A98A03 CRC64;  
  
Query Match 2.7%; Score 9; DB 11; Length 335;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 138 QSNKNGTCV 146  
DB 135 QSNKNGTCV 143  
  
RESULT 13  
Q884T6 PRELIMINARY; PRT; 83 AA.  
ID Q884T6;  
AC Q884T6;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DE Prevent-host-death family protein.  
GN PSP02000.

OS Pseudomonas syringae (pv. tomato).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OK NCBI\_TaxID=323;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DC3000;  
 RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,  
 RA Berry K., Uteerback T., Van Aken S., Feldblyum T., Gwinn M.,  
 RA Dodson R., Debroy R., Dukkin A., Kolonay J., Madupu R., Daugherty S.,  
 RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,  
 RA White O., Fraser C., Collier A.;  
 RT "Complete sequence of Pseudomonas syringae."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB016862; AA055518.1; -.  
 DR TIGR; PSP02000; -.  
 KW Complete proteome.  
 SQ SEQUENCE 83 AA; 8993 MW; ED9080CB44BCD3EE CRC64;

Query Match 2.4%; Score 8; DB 16; Length 83;  
 Best Local Similarity 100.0%; Pred. No. 6.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 QLTGSAAS 23  
 |||||  
 Db 46 QLTGSAAS 53

## RESULT 14

Q94E37 PRELIMINARY; PRT; 91 AA.  
 AC Q94E37;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE OSUNB0032H19.17 proteIn.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OK NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC  
 clone:OSUNB0032H19." to the EMBL/GenBank/DBJ databases.  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP003219; BAB61185.1; -.  
 DR Gramene; Q94E37; -.  
 SQ SEQUENCE 91 AA; 9789 MW; D9D559FB49BF71B2 CRC64;

Query Match 2.4%; Score 8; DB 10; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 6.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 LLLSLFVL 243  
 |||||  
 Db 16 LLLSLFVL 23

## RESULT 15

Q81VU0 PRELIMINARY; PRT; 129 AA.  
 AC Q81VU0;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Similar to papilin, proteoglycan-like sulfated glycoprotein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Plimates; Catarrhini; Homnidae; Homo.  
 OK NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RA Strausberg R.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC042057; AA042057.1; -.  
 DR InterPro; IPR000884; TSP1.  
 DR Pfam; PF01090; TSP\_1; 1.  
 DR PRINTS; P101705; TSP1REPEAT.  
 DR SMART; SM00209; TSP1; 1.  
 DR PROSITE; PS50092; TSP1; 1.  
 SQ SEQUENCE 129 AA; 14368 MW; D51144A494C12B3B CRC64;

Query Match 2.4%; Score 8; DB 4; Length 129;  
 Best Local Similarity 100.0%; Pred. No. 9.3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 LLLVPLLL 238  
 |||||  
 Db 4 LLLVPLLL 11

Search completed: August 18, 2004, 16:16:37  
 Job time : 42 secs